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OM protein - protein search, using sw model

Run on: March 1, 2006, 02:42:12 ; Search time 81 Seconds
(without alignments)
48.820 Million cell updates/sec

Title: US-09-583-200F-22

Perfect score: 41

Sequence: 1 RLQETELV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	9	2 AAR59123	Aar59123 Peptide f
2	41	100.0	9	2 Aaw36829	Aaw36829 Immunogen
3	41	100.0	9	2 Aaw70055	Aaw70055 HER-2/neu
4	41	100.0	9	4 Aab99701	Aab99701 HLA A2 bi
5	41	100.0	9	4 Aag88770	Aag88770 HER2/neu
6	41	100.0	9	4 Aag89002	Aag89002 HER2/neu
7	41	100.0	9	5 ABG79079	ABG79079 Human HER
8	41	100.0	9	5 AAE26825	AAE26825 Human HER
9	41	100.0	9	5 AAE31139	AAE31139 Human erb
10	41	100.0	9	5 AEA36331	AEA36331 Human EGF
11	41	100.0	9	7 ADA49636	ADA49636 Multi-epi
12	41	100.0	9	7 ABO07298	ABO07298 Cytotoxic
13	41	100.0	9	7 ABW00310	ABW00310 HER-2 HLA
14	41	100.0	9	8 ADE97585	ADE97585 Immunogen
15	41	100.0	9	8 ADG89645	ADG89645 Class I H
16	41	100.0	9	8 ADM12641	ADM12641 MHC class
17	41	100.0	9	8 ADM12635	ADM12635 MHC class
18	41	100.0	9	8 ADO24294	ADO24294 Unidentif
19	41	100.0	9	8 ADO38874	ADO38874 Human Her
20	41	100.0	9	8 ADP79772	ADP79772 Human HLA
21	41	100.0	9	8 ADU04945	ADU04945 HER-2/neu
22	41	100.0	9	9 ADU66573	ADU66573 Cancer-as
23	41	100.0	9	9 ADW88104	ADW88104 Human HER
24	41	100.0	9	9 ADX08595	ADX08595 Class I H

25	41	100.0	9	9 ADZ40816	Adz40816 Multi-epi
26	41	100.0	15	3 AAY98954	Aay98954 HLA class
27	41	100.0	15	4 AAG89088	Aag89088 HER2/neu
28	41	100.0	15	4 AAG88588	Aag88588 HER2/NEU
29	41	100.0	15	4 AAG88704	Aag88704 HER2/NEU
30	41	100.0	16	9 ADW88101	Adw88101 Human HER
31	41	100.0	36	8 ADJ32563	Adj32563 Human erb
32	41	100.0	144	7 ADA49445	Ada49445 Multi-epi
33	41	100.0	144	8 ADO24123	Ado24123 Epigene c
34	41	100.0	144	9 ADZ40625	Adz40625 BCL A2 #8
35	41	100.0	147	7 ADA49447	Ada49447 Multi-epi
36	41	100.0	147	8 ADO24125	Ado24125 Epigene c
37	41	100.0	147	9 ADZ40627	Adz40627 BCL A2 #6
38	41	100.0	148	7 ADA49443	Ada49443 Multi-epi
39	41	100.0	148	8 ADO24121	Ado24121 Epigene c
40	41	100.0	148	9 ADZ40623	Adz40623 BCL A2 #9
41	41	100.0	391	9 AEA39008	Aea39008 Rat Her-2
42	41	100.0	435	8 ADR10480	Adr10480 Human pro
43	41	100.0	470	9 ADY30515	Ady30515 Human spl
44	41	100.0	583	5 AAE20483	Aae20483 Human pro
45	41	100.0	587	5 AAE20481	Aae20481 Human pro

ALIGNMENTS

RESULT 1

AAR59123

ID AAR59123 standard; peptide; 9 AA.

XX AC AAR59123;

XX DT 25-MAR-2003 (revised)

DT 02-MAY-1995 (first entry)

XX DE Peptide fragment (1.0330) of

XX KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBV; EBV; HIV1; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO9420127-A1.

XX PD 15-SEP-1994.

XX PF 04-MAR-1994; 94WO-US002353.

XX PR 05-MAR-1993; 93US-00027146.

PR 04-JUN-1993; 93US-00073205.

PR 29-NOV-1993; 93US-00159184.

XX PA (CYTE-) CYTEL CORP.

XX PI Grey HM, Sette A, Sidney J, Kast W;

XX WPI; 1994-302678/37.

XX DR Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.

XX PS Example 5; Page 100; 138pp; English.

XX CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (AAR71293). AAR59123 has an IC50 of 0.091 and the sequence occurs at position 689 in the C-ERB2 protein. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the

CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 41; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLLOTELV 9
 Db |||||
 1 RLLOTELV 9

RESULT 2
 AAW36829
 ID AAW36829 standard; peptide; 9 AA.
 XX
 AC AAW36829;
 XX
 DT 23-MAR-1998 (first entry)
 XX
 DE Immunogenic peptide H13 based on the human Her-2/neu protein.
 XX
 KW Her-2/neu protein; human leukocyte antigen A2.1; HLA;
 KW cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;
 KW T-cell receptor; TCR; tumour treatment.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX WO9732603-A1.
 PN
 XX 12-SEP-1997.
 PD
 XX
 PF 05-MAR-1997; 97WO-US003611.
 XX
 XX
 PR 05-MAR-1996; 96US-0012845P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Sherman LA, Lustgarten J;
 PI
 XX WPI; 1997-470496/43.
 DR
 XX Nucleic acid encoding variable regions of HLA-restricted non-human T cell
 PT receptor specific for tumour antigen - used to identify tumour antigens
 PT and for tumour therapy.
 XX
 XX Example 1; Page 9; 34pp; English.

CC Synthetic peptides AAW36824-40 are based on the sequence of the human Her
 CC -2/neu protein, wherein each sequence contains the anchor motif for human
 CC leukocyte antigen (HLA) A2.1. The present peptide is based on positions
 CC 699-697. The ability of these peptides to inhibit the binding of an
 CC influenza virus matrix protein peptide M1 to HLA A2.1 was measured by
 CC inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic T
 CC lymphocyte (CTL) clone. The present protein showed 56% inhibition. The
 CC peptides were also tested for their ability to elicit an immune response
 CC in vivo. However, only H3 (AAW36824) and H7 (AAW36826) were able to do
 CC this. H3 and H7 peptides are tumour-associated antigens, and were used to
 CC immunize a transgenic, non-human vertebrate (that has been modified to
 CC express at least one HLA antigen), so that the animal produces CTL which
 CC displays HLA-restricted T-cell receptor (TCR) specificity for the
 CC antigen. Nucleic acid encoding variable regions of the alpha and beta
 CC chains of such TCRs can be amplified from CTLs produced in the above
 CC manner. Cells expressing recombinant TCR are used to identify antigens
 CC associated with a tumour and to treat tumours in humans. Transgenic mice
 CC are a more convenient source of CTL than the tumour-infiltrating
 CC lymphocytes previously used. TCR can be humanised to reduce side-
 CC reactions and short peptide derivatives of TCR are more economical to
 CC produce than TCR itself, particularly when expressed as a single-chain
 CC molecule rather than as a dimer

XX Sequence 9 AA;
 SQ Query Match 100.0%; Score 41; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLLOTELV 9
 Db |||||
 1 RLLOTELV 9

RESULT 3
 AAW70055
 ID AAW70055 standard; peptide; 9 AA.
 XX
 AC AAW70055;
 XX
 DT 22-OCT-1998 (first entry)
 XX
 DE HER-2/neu derived HLA-A2.1 binding peptide 3 (residues 689-697).
 XX
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;
 KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX WO9833888-A1.
 PN
 XX 06-AUG-1998.
 PD
 XX
 PF 30-JAN-1998; 98WO-US001959.
 XX
 XX
 PR 31-JAN-1997; 97US-0036696P.
 XX
 XX (EPIM-) EPIMUNE INC.
 PA
 XX Tsai V, Southwood S, Sidney J, Sette A, Celis E;
 PI
 XX WPI; 1998-437445/37.
 DR
 XX Production of antigen-specific cytotoxic T cells - by incubating
 PT immunogenic peptide(s) from antigen that binds class I major
 PT histocompatibility complex molecules with pre-treated antigen presenting
 PT cells.
 XX
 XX Example 7; Page 77; 104pp; English.

Sequences shown in AAW70053 to AAW70075 represent peptides derived from
 HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte
 antigen (HLA) , HLA-A2.1 and are used to exemplify the method of invention
 of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The
 method comprises contacting immunogenic peptides from an antigen that
 binds class I major histocompatibility complex (MHC) molecules with
 antigen presenting cells (APCs) pretreated with pretreatment growth
 factors, and incubating the APCs with purified CD8 cells in the presence
 of at least 2 incubation growth factors, thereby producing antigen-
 specific CTLs. A method for specifically killing target cells in a human
 patient is also provided which comprises obtaining a fluid sample
 containing CTLs from a patient, contacting the cytotoxic T cells with
 APCs pretreated with pre-treatment growth factors, where the APCs
 comprise class I MHC molecules. The pretreated APCs are incubated with
 the cytotoxic growth factors, thereby producing activated CTLs which are
 contacted with a carrier to form a composition. The composition can then
 be administered to the patient. The activated CTLs can be used for
 treating cancers, immune disorders, viral infections, AIDS, hepatitis,
 bacterial infection, fungal infection, malaria or tuberculosis

XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9
Db 1 RLLQETELV 9

RESULT 4
AAB99701
ID AAB99701 standard; peptide; 9 AA.
XX AC AAB99701;
XX 06-SEP-2001 (first entry)
XX HLA A2 binding CTL epitope peptide from Her2/neu SEQ ID NO:22.
XX Human leukocyte antigen A2 binding peptide; HLA class I A2; CTL;
KW cytotoxic T-cell lymphocyte; tumour associated antigen; CEA; HER2/neu;
KW MAGE3; P53; vaccine; cancer; cytostatic; immunomodulator;
KW immunotherapy; immune response.
XX Homo sapiens.
XX WO200141741-A1.
XX 14-JUN-2001.
XX 13-DEC-2000; 2000WO-US034318.
XX 13-DEC-1999; 99US-0170448P.
PR 05-APR-2000; 2000US-00543608.
PR 30-MAY-2000; 2000US-00583200.
XX (EPIM-) EPIMMUNE INC.
XX Fikes J, Sette A, Sidney J, Southwood S, Celis E, Keogh E;
PI Chesnut R;
XX WPI; 2001-381489/40.
XX Compositions for use in a vaccine for treating, e.g., breast, lung and
PT colon cancer comprises at least one peptide that comprises an isolated
PT epitope of a tumor-associated antigen.
XX Claim 1; Page 76; 86pp; English.

CC The present invention describes a composition (I) comprising at least one
CC peptide that comprises an isolated, prepared epitope consisting of a
CC sequence selected from 25 short amino acid sequences given in AAB99680 to
CC AAB99704. Also described are: (1) a composition (II) comprising one or
CC more peptides, and further comprising at least two epitopes selected from
CC the 25 short amino acid sequences (as above), where each of the one or
CC more peptides comprise less than 50 contiguous amino acids that have 100%
CC identity with a native peptide sequence; and (2) a vaccine composition
CC (III) comprising an epitope selected from the 25 short amino acid
CC sequences (as above) and a pharmaceutical excipient. (I) has cytostatic
CC and immunomodulatory activities and can be used in vaccine production and
CC immunotherapy. The peptide epitope compositions (I)-(II) are useful for
CC monitoring an immune response to a tumour associated antigen or when one
CC or more peptides are combined to create a vaccine (III) that stimulates
CC the cellular arm of the immune system. In particular, the vaccine
CC mediates immune responses against tumours in individuals who bear an
CC allele of the human leukocyte antigen (HLA)-A2 supertype and improve the
CC standard of care for patients being treated for breast, colon, or lung
CC cancer
XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9
Db 1 RLLQETELV 9

RESULT 5
AAG88770
ID AAG88770 standard; peptide; 9 AA.
XX AC AAG88770;
XX 11-SEP-2001 (first entry)
XX HER2/neu A2 supermotif crossbinding peptide #14.
XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX Homo sapiens.
XX Synthetic.
XX WO200141787-A1.
XX 14-JUN-2001.
XX 11-DEC-2000; 2000WO-US033591.
XX 10-DEC-1999; 99US-00458299.
XX (EPIM-) EPIMMUNE INC.
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
PI Keogh E;
XX WPI; 2001-374995/39.
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
XX Example 2; Page 179; 199pp; English.

CC The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines for the
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample form a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention
XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
| | | | |
Db 1 RLLQETELV 9

RESULT 6
AAG89002
ID AAG89002 standard; peptide; 9 AA.
AC AAG89002;
XX
DT 11-SEP-2001 (first entry)
XX
DE HER2/neu epitope HLA-A2 supermotif-bearing peptide #15.
XX
KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200141787-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033591.
XX
PR 10-DEC-1999; 99US-00458299.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
PI Keogh E;
XX
WPI; 2001-374995/39.
XX
XX
XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
PT cellular immune responses for the prevention and treatment of cancer.
PS
PS Claim 1; Page 189; 199pp; English.
XX
XX The present invention describes isolated prepared HER2/neu epitopes (I).
CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
CC culture in vitro and binds to a complex of an epitope (I), bound to a
CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
CC and a second epitope and the peptide is less than 50 contiguous amino
CC acids that have 100% identity with a native peptide sequence of HER2/neu;
CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)
CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and
CC immunostimulant activities, and can be used in vaccines. (I), (II) and
CC (III) are useful for inducing cellular immune responses for the
CC prevention and treatment of cancer. (I) and (II) are useful for
CC monitoring or evaluating an immune response to a tumour-associated
CC antigen when incubated with a T lymphocyte sample from a patient and
CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
CC based vaccines mean that immunosuppressive epitopes that may be present
CC in whole antigens may be avoided. Selected epitopes may be combined to
CC enhance immunogenicity. The possible pathological side effects caused by
CC infectious agents or whole protein antigen is eliminated. The vaccine
CC provides the ability to direct and focus an immune response to multiple
CC selected antigens from the same pathogen. Epitope-based anti-tumour
CC vaccines provides the opportunity to combine epitopes derived from
CC multiple tumour-associated molecules addressing the problem of tumour-
CC tumour variability and reducing the likelihood of tumour escape due to
CC antigen loss. AAG89266 to AAG89121 represent amino acid sequences used in
CC the exemplification of the present invention

XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
| | | | |
Db 1 RLLQETELV 9

RESULT 7
ABG79079
ID ABG79079 standard; peptide; 9 AA.
XX
AC ABG79079;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human HER-2 class I HLA widely expressed antigen peptide #3.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
WPI; 2002-627577/67.
XX
XX Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 17; 61pp; English.
XX
XX The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
CC The animal is further subjected to a cancer treatment including surgery,
CC radiation, chemotherapy or gene therapy. The administration of (I),
CC preferably dendritic cell is prior to, subsequent to or concurrent with,

CC the cancer treatment. The present sequence is a tumour antigen derived
CC epitope for inclusion in the composition of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
| | | | |
Db 1 RLQETELV 9

RESULT 8

AAE26825
ID AAE26825 standard; peptide; 9 AA.

XX

AC AAE26825;

XX DT 13-DEC-2002 (first entry)

XX Human HER-2/neu peptide.

XX Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;

XX epitope; HER-2/neu.

XX Homo sapiens.

XX WO200265992-A2.

XX 29-AUG-2002.

XX 19-FEB-2002; 2002WO-US005748.

XX 20-FEB-2001; 2001US-0270252P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;

XX Heiskala M;

XX WPI; 2002-667033/71.

XX Treating a subject with cancer comprises combining the CD+8 cells, which

XX are stimulated with non-naturally occurring antigen-presenting cell line,

XX with adherent blood monocytes and inoculating the subject with CD8+

XX suspension.

XX Example 3; Page 98; 99pp; English.

XX The invention relates to a method of treating a subject with cancer. The

XX method involves combining the CD+8 cells, which are stimulated with non

XX naturally occurring antigen-presenting cell (mAPC) line, with adherent

XX blood monocytes and inoculating the subject with CD8+ suspension. The

XX method is useful for treating cancer e.g. ovarian cancer, breast cancer

XX and melanoma etc. It is also useful in cell therapy. The present sequence

XX is human HER-2/neu peptide used to illustrate method of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9

| | | | |

Db 1 RLQETELV 9

RESULT 9

AAE31139

ID AAE31139 standard; peptide; 9 AA.

XX AAE31139;
XX 24-FEB-2003 (first entry)
XX Human erb2 peptide #24.
XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
XX Homo sapiens.
XX WO200272627-A2.
XX 19-SEP-2002.
XX 11-MAR-2002; 2002WO-EP002666.
XX 09-MAR-2001; 2001US-0274250P.
XX 14-MAY-2001; 2001US-0290353P.
XX 18-MAY-2001; 2001US-0291610P.
XX (CALL-) CALLISTOGEN AG.
XX Wrede P, Walden P, Eichler-Mertens M, Filter M;
XX WPI; 2002-759836/82.
XX Providing, identifying or optimizing peptides for inducing cytotoxic T-
XX lymphocytes and for treating cancer, comprises selecting conserved in the
XX regions in antigenic proteins and identifying CD8+ T-cell epitopes in the
XX protein.
XX Disclosure; Page 8; 32pp; English.
XX The invention relates to a method for providing, identifying or/and
XX optimising peptides which induce cytotoxic T-lymphocytes and to the uses
XX of the obtained peptides for vaccination. The method is useful for
XX providing, identifying and/or optimising peptides that are useful in
XX manufacturing a pharmaceutical composition for the induction of cytotoxic
XX T-lymphocytes, and for the prevention, treatment or diagnosis of cancer
XX or viral infections. The invention is also used in gene therapy. The
XX present sequence is human erb2 peptide used to illustrate the method of
XX the invention
XX Sequence 9 AA;
XX Query Match 100.0%; Score 41; DB 5; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 RLQETELV 9
XX | | | | |
XX Db 1 RLQETELV 9
XX RESULT 10
XX AEA36331
XX ID AEA36331 standard; peptide; 9 AA.
XX AC AEA36331;
XX 11-AUG-2005 (first entry)
XX Human EGFR cytotoxic T-lymphocyte epitope peptide - SEQ ID 41.
XX viral infection; virucide; cytostatic; tumor; neoplasm; cell therapy;
XX antigen; Endothelial growth factor receptor; EGFR.
XX Homo sapiens.
XX JP2005139118-A.
XX 02-JUN-2005.

XX PF 07-NOV-2003; 2003JP-00377653.
 XX PR 20-FEB-2001; 2001US-0270252P.
 XX PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX PI Leturco DJ, Moriarty AM, Jackson MR, Peterson PA, Richards JM;
 XX DR WPI; 2002-667033/71.
 XX XX Treating a subject with cancer comprises combining the CD+8 cells, which
 PT are stimulated with non-naturally occurring antigen-presenting cell line,
 PT with adherent blood monocytes and inoculating the subject with CD8+
 PT suspension.
 XX XX Example 3; SEQ ID NO 41; 65pp; Japanese.
 XX XX The invention relates to a novel method for treating viral infection in a
 CC subject. The method comprises preparing an antigen presentation cell
 CC lineage (nnAPC), collecting CD8+ cells from the subject, stimulating CD8+
 CC cells using the nnAPC, culturing CD8+ cells in the presence of
 CC interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from
 CC the subject, subjecting the components to gamma irradiation, combining
 CC the CD8+ cells with adhesive peripheral blood monocytes and inoculating
 CC the CD8+ suspended solid to the subject. The method of the invention
 CC demonstrates virucide and cytostatic activities and may be useful for
 CC treating a viral infection or tumor in a subject via cell therapy. The
 CC current sequence is that of a human EGFR cytotoxic T-lymphocyte epitope
 CC peptide of the invention which was incorporated into a Drosophila antigen
 CC presenting cell.
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 41; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLQETELV 9
 DB 1 RLQETELV 9
 RESULT 11
 ADA49636
 ID ADA49636 standard; peptide; 9 AA.
 XX AC ADA49636;
 XX DT 20-NOV-2003 (first entry)
 XX DE Multi-epitope construct specific epitope #178.
 XX KW multi-epitope; immunogenic; epitope; major histocompatibility complex;
 KW MHC class I; MHC class II; junctional epitope.
 XX OS Unidentified.
 XX US2002119127-A1.
 XX 29-AUG-2002.
 XX 27-JUN-2001; 2001US-00894018.
 XX 28-DEC-1999; 99US-0173390P.
 XX 28-DEC-2000; 2000WO-US035568.
 XX 16-APR-2001; 2001US-0284221P.
 XX (SETT/) SETTE A.
 PA (CHES/) CHESNUT R.
 PA (LIVI/) LIVINGSTON B. D.
 PA (BAKE/) BAKER D. M.
 PA (NEWM/) NEWMAN M. J.

PA (BROW/) BROWN D. H.
 XX Sette A, Chesnut R, Livingston BD, Baker DM, Newman MJ, Brown DH;
 XX WPI; 2003-615704/58.
 XX PT Designing multi-epitope construct having major histocompatibility complex
 PT class I and II epitope nucleic acids, by selecting mixture of amino acid
 PT insertions at junctions of construct to minimize junctional epitopes.
 XX XX Disclosure; Fig 19D; 78pp; English.
 XX XX The invention relates to a method of designing multi-epitope constructs
 CC comprising major histocompatibility complex (MHC) class I and II (CTL)
 CC epitope nucleic acids (CEN), involves sorting CEN, introducing flanking
 CC amino acid residue selected from specified amino acid residues given in
 CC specification at C+1 position of CEN, introducing amino acid spacer
 CC residues between two CEN, and selecting the constructs having less
 CC junctional epitopes. The method is useful for designing a multi-epitope
 CC construct having multiple epitope nucleic acid. The method avoids or
 CC minimises the occurrence of junctional epitopes and maximises the
 CC immunogenicity and/or antigenicity of multi-epitope vaccines. The present
 CC sequence represents the amino acid sequence of an epitope present in a
 CC multi-epitope construct.
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 41; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLQETELV 9
 DB 1 RLQETELV 9
 RESULT 12
 ABO07298
 ID ABO07298 standard; peptide; 9 AA.
 XX AC ABO07298;
 XX DT 13-AUG-2003 (first entry)
 XX DE Cytotoxic T-lymphocyte (CTL)-stimulating peptide #26.
 XX KW Human; HER-2/neu proto-oncogene; HER-2; cytotoxic T-lymphocyte; CTL;
 KW CTL-stimulating peptide; immune response; breast cancer;
 KW proliferative disorder; ovarian cancer; anti-cancer vaccine;
 KW molecular weight standard; chromatographic column; cytostatic.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN US6514942-B1.
 XX PD 04-FEB-2003.
 XX 14-MAR-1995; 95US-00403459.
 XX 14-MAR-1995; 95US-00403459.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Ioannides CG, Fisk BA, Ioannides MG;
 XX WPI; 2003-465587/44.
 XX PT New HER-2/neu protooncogene (Her-2) peptides, useful for stimulating
 PT cytotoxic T-lymphocytes to generate immune responses against epitopes of
 PT protooncogenes, or for treating or diagnosing e.g. breast or ovarian
 PT cancers.
 XX XX

PS Example 2; Col 42; 57pp; English.

CC The present invention relates to peptides which induce human HER-2/neu
 CC proto-oncogene (HER-2) peptide reactive cytotoxic T-lymphocytes (CTL).
 CC The peptides are referred to a CTL-stimulating peptides. The peptides are
 CC useful for stimulating cytotoxic T-lymphocytes and generating immune
 CC responses against epitopes of proto-oncogenes. The peptides are
 CC particularly useful for treating or diagnosing various proliferative
 CC disorders (e.g. breast or ovarian cancers), or for producing anti-cancer
 CC vaccines. The peptides may also be used as standards in the
 CC identification of small molecular-weight polypeptides, for the
 CC calibration and standardisation of chromatographic columns used in the
 CC separation of low-molecular-weight polypeptides, or as protein
 CC -stimulating standards in reactions. ABO07273-ABO07301 represent the CTL
 CC -stimulating peptides of the invention

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
 Db 1 RLLQETELV 9

RESULT 13

ABW00310
 ID ABW00310 standard; peptide; 9 AA.

AC ABW00310;

DT 15-JAN-2004 (first entry)

DE HER-2 HLA-A2 anchor peptide, HER-2:689-697.

KW Tumour-associated antigen; proliferative disorder; cancer; vaccine;
 KW gene therapy; cytostatic; HER-2.

OS Unidentified.

PN US2003027766-A1.

PD 06-FEB-2003.

PF 31-OCT-2001; 2001US-00001546.

PR 14-MAR-1995; 95US-00403459.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Ioannides CG, Fisk BA, Ioannides MG;

DR WPI; 2003-765297/72.

XX New HER-2/neu peptide that binds human leukocyte antigen and stimulates
 PT cytotoxic T-lymphocytes, useful for diagnosing and/or treating
 PT proliferative disorders, e.g. cancer, and for producing potential anti-
 PT cancer vaccines.

PS Claim 4; Page 23; 59pp; English.

XX The present invention relates to a new tumour-associated antigen (HER-2/
 CC neu peptide that binds human leukocyte antigen and stimulates cytotoxic T
 CC -lymphocytes. The invention is useful for stimulating T-lymphocytes and
 CC generating immune responses against epitopes of proto-oncogenes. These
 CC are used for diagnosing and treating proliferative disorders such as
 CC cancer and in producing potential anti-cancer vaccines. The invention is
 CC also useful in gene therapy. The present sequence is HER-2 HLA-A2 anchor
 CC peptide

XX Sequence 9 AA;

Query Match 100.0%; Score 41; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
 Db 1 RLLQETELV 9

RESULT 14
 ADE97585
 ID ADE97585 standard; peptide; 9 AA.

XX ADE97585;
 XX
 DT 12-FEB-2004 (first entry)

XX Immunogenic HLA-A2.1 binding peptide #67.

KW cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;
 KW immunogenic peptide composition; immune response; prostate cancer;
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;
 KW human leukocyte antigen A2.1; HLA A2.1;
 KW immunogenic HLA-A2.1 binding peptide.

XX Synthetic.

XX US2003185822-A1.

XX 02-OCT-2003.

XX 03-APR-2002; 2002US-00116557.

XX 05-MAR-1993; 93US-00027146.

XX 04-JUN-1993; 93US-00073205.

XX 29-NOV-1993; 93US-00159184.

XX 02-DEC-1994; 94US-00349177.

XX (GREY/) GREY H M.

XX (SETT/) SETTE A.

XX (SIDN/) SIDNEY J.

XX Grey HM, Sette A, Sidney J;

XX WPI; 2004-041186/04.

XX Immunogenic peptide composition for preventing, treating or diagnosing
 PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired
 PT immunodeficiency Syndrome, and renal carcinoma, includes conserved
 PT residues at specified positions.

XX Example 11; Page 23; 38pp; English.

XX The invention describes an immunogenic peptide composition comprising 9
 CC residues including a first conserved residue at a second position from N-
 CC terminus, and a second conserved residue at C-terminal position. The
 CC inventive peptide composition is used to elicit an immune response
 CC against a desired antigen for preventing, treating or diagnosing
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune

CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,
CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic
CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing
CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,
CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,
CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic
CC purpura, Grave's disease, and Addison's disease. The invention defines
CC positions within a motif enabling the selection of the peptides, which
CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the
CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.
XX
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
| | | | |
Db 1 RLQETELV 9

RESULT 15

ADG89645
ID ADG89645 standard; peptide; 9 AA.

XX AC ADG89645;

XX DT 11-MAR-2004 (first entry)

XX DE Class I HLA-restricted widely expressed antigen #10.

XX KW metastatic cancer cell differentiation; mutated fibronectin;

XX KW metastatic cancer; class I HLA-restricted; widely antigen.

XX OS Unidentified.

XX PN WO2003100027-A2.

XX PD 04-DEC-2003.

XX PF 28-MAY-2003; 2003WO-US016736.

XX PR 28-MAY-2002; 2002US-0383530P.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Wang R;

XX WPI; 2004-035134/03.

XX PT Identifying a cell that differentiates into a metastatic cancer cell,
XX PT useful for preventing metastatic cancer, comprises identifying a mutated
XX PT fibronectin in the cell.

XX PS Disclosure; SEQ ID NO 88; 137pp; English.

XX CC The invention comprises a method for identifying a cell that will
XX CC differentiate into a metastatic cancer cell, the method involves
XX CC identifying a mutated fibronectin in the cell. The method of the
XX CC invention is useful for preventing metastatic cancer. The present amino
XX CC acid sequence represents a Class I HLA-restricted widely expressed
XX CC antigen.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
| | | | |
Db 1 RLQETELV 9

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OM protein - protein search, using sw model

Run on: March 1, 2006, 02:48:52 ; Search time 39 Seconds
(without alignments)
22.204 Million cell updates/sec

Title: US-09-583-200F-22

Perfect score: 41

Sequence: 1 RLLOQTELV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	1254	2 I48161	p-185 precursor -
2	41	100.0	1255	1 A24571	protein-tyrosine k
3	41	100.0	1260	1 TVRTNU	protein-tyrosine k
4	35	85.4	540	1 TVFVEB	protein-tyrosine k
5	35	85.4	540	2 B44776	protein-tyrosine k
6	35	85.4	544	2 S35745	protein-tyrosine k
7	35	85.4	545	2 S00727	kinase-related tra
8	35	85.4	565	2 T46251	hypothetical prote
9	35	85.4	604	1 TVVYUH	protein-tyrosine k
10	35	85.4	698	1 TVFVLV	protein-tyrosine k
11	35	85.4	955	1 T33040	hypothetical prote
12	35	85.4	1210	1 GQHU5	epidermal growth f
13	35	85.4	1210	2 A53183	epidermal growth f
14	35	85.4	1223	1 TVCHLV	epidermal growth f
15	33	80.5	46	2 I52716	gene neu protein -
16	32	78.0	416	2 E69599	competence-damage
17	32	78.0	434	2 C71418	cytochrome P450 -
18	32	78.0	477	2 F84667	probable cytochrom
19	32	78.0	498	2 F84667	probable cytochrom
20	32	78.0	509	2 C85169	cytochrome P450 li
21	32	78.0	514	2 E84667	probable cytochrom
22	32	78.0	515	2 H71417	cytochrome P450 -
23	32	78.0	519	2 A96542	probable cytochrom
24	32	78.0	527	1 A71418	cytochrome P450 d1
25	32	78.0	678	2 A54514	glutamic acid-rich
26	32	78.0	738	2 A48246	ethylene-response
27	32	78.0	738	2 T01897	ethylene-response
28	32	78.0	740	2 T51619	probable ethylene
29	32	78.0	741	2 T16992	ethylene receptor

RESULT 1
I48161
P-185 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I48161
R:Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa, K.
Gene 140, 251-255, 1994
A:Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A:Reference number: I48161; MUID:94193007; PMID:7908275
A:Accession: I48161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1254 <RSS>
A:Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; NID:G4932336; PIDN:
C:Genetics:
A:Gene: neu
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C:Keywords: ATP
F:718-983/Domain: protein kinase homology <KIN>
F:726-734/Region: protein kinase ATP-binding motif

ALIGNMENTS

Query Match 100.0%; Score 41; DB 2; Length 1254;
Best Local Similarity 100.0%; Pred.No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLLOQTELV 9
Db 689 RLLOQTELV 697
RESULT 2
A24571
protein-tyrosine kinase (BC 2.7.1.112) erbB2 precursor - human
N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erb
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
C:Accession: A24571; A25491; A44188; B44188; I59509; I57622
R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f
A:Reference number: A24571; MUID:86118663; PMID:3003577
A:Accession: A24571
A:Molecule type: mRNA
A:Residues: 1-1255 <YAM>
A:Cross-references: UNIPROT:P04626; UNIPARC:UPI000003F55F; GB:X03363; NID:G31197; PIDN:
R:Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epider
A:Reference number: A25491; MUID:86016729; PMID:2995967
A:Accession: A25491
A:Molecule type: DNA

A;Residues: 737-1031 <SBM>
A;Cross-references: UNIPARC:UPI000016A8A7; GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:
R;Cousens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P.
Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos
A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188
A;Molecule type: DNA
A;Residues: 740-910 <COU1>
A;Cross-references: UNIPARC:UPI000016AA26; GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:
A;Accession: B44188
A;Molecule type: mRNA
A;Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A;Cross-references: UNIPARC:UPI00001725C7; GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Accession: I59509
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 832-909 <REX>
A;Cross-references: UNIPARC:UPI0000070A3F; GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional
A;Reference number: I57622; MUID:87286898; PMID:3039351
A;Accession: I57622
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-191 <TAL>
A;Cross-references: UNIPARC:UPI0000000427; GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 30
C;Genetics:
A;Gene: GDB:ERBB2; NGL; NEU; HER-2
A;Cross-references: GDB:120613; OMIM:164870
A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph
inase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;70-304/Domain: EGF receptor extracellular domain repeat <EE1>
F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>
F;654-675/Domain: transmembrane #status predicted <TM>
F;676-1255/Domain: intracellular #status predicted <INT>
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif
F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predict
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 100.0%; Score 41; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. NO. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLOETELV 9
|||||
Db 689 RLLOETELV 697

RESULT 3
TVRTNU

protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C;Accession: A24562; A61204

R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The new oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: UNIPROT:P06494; UNIPARC:UPI0000161B83; EMBL:X03362; NID:g56745; PID:
R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no
2-thiazolylformamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
A;Accession: A61204
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 637-663, 'V', 665-702 <MAS>
A;Cross-references: UNIPARC:UPI00001725C8
A;Note: authors translated the codon GCA for residue 25 as Val
C;Genetics:
A;Gene: neu
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F;658-680/Domain: transmembrane #status predicted <TM>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted
Query Match 100.0%; Score 41; DB 1; Length 1260;
Best Local Similarity 100.0%; Pred. NO. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLLOETELV 9
|||||
Db 694 RLLOETELV 702

RESULT 4
TVFVEB

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)
C;Species: avian erythroblastosis virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: A25231; B25231
R;Choi, O.R.; Trainor, C.; Graf, T.; Beug, H.; Engel, J.D.
Mol. Cell. Biol. 6, 1751-1759, 1986
A;Title: A single amino acid substitution in v-erbB confers a thermolabile phenotype to
A;Reference number: A25231; MUID:87064458; PMID:2878364
A;Accession: A25231
A;Molecule type: DNA
A;Residues: 1-540 <CHO>
A;Cross-references: UNIPROT:PI1273; UNIPARC:UPI000017100D; GB:M13179; NID:g209679; PIDN
A;Note: the authors translated the codon AAG for residue 157 as Gly, ATG for residue 25.
C;Genetics:
A;Gene: erbB
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F;130-395/Domain: protein kinase homology <KIN>
F;138-146/Region: protein kinase ATP-binding motif
F;165/Active site: Lys #status predicted

Query Match 85.4%; Score 35; DB 1; Length 540;
Best Local Similarity 88.9%; Pred. NO. 20;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLLOETELV 9
|||||
Db 101 RLLOETELV 109

RESULT 5
B44776
protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)
C:Species: avian erythroblastosis virus
C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 31-Dec-2004
C:Accession: B44776
R:Bruckin, A.; Jackson, J.; Bishop, J.M.; McCarley, D.J.; Schatzman, R.C.
Oncogene 5, 15-24, 1990
A>Title: Six amino acids from the retroviral gene gag greatly enhance the transforming p
A:Reference number: A44776; MUID:90206603; PMID:1969616
A:Accession: B44776
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-540 <BRU>
A:Cross-references: UNIPROT:Q85468; UNIPROT:Q64895; UNIPARC:UPI000017561D; GB:X52211
C:Genetics:
A:Gene: erbB
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:130-395/Domain: protein kinase homology <KIN>
F:138-146/Region: protein kinase ATP-binding motif

Query Match 85.4%; Score 35; DB 2; Length 540;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
|||||
Db 101 RLLOQERELV 109

RESULT 6
S35745
protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus
C:Species: avian erythroblastosis virus
C>Date: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S35745
R:Vennstroem, B.
submitted to the EMBL Data Library, March 1993
A:Reference number: S35743
A:Accession: S35745
A:Molecule type: DNA
A:Residues: 1-544 <VEN>
A:Cross-references: UNIPROT:Q85468; UNIPROT:Q64895; UNIPARC:UPI000017561F; EMBL:X12707
C:Genetics:
A:Gene: erbB
C:Superfamily: protein kinase homology
C:Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific p
F:135-400/Domain: protein kinase homology <KIN>
F:143-151/Region: protein kinase ATP-binding motif
F:170/Active site: Lys #status predicted

Query Match 85.4%; Score 35; DB 2; Length 544;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
|||||
Db 106 RLLOQERELV 114

RESULT 7
S00727
kinase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis virus
C:Species: avian erythroblastosis virus
C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Dec-2004
C:Accession: S00727
R:Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.
Oncogene Res. 1, 265-278, 1987
A>Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mutant
A:Reference number: S00727; MUID:88217326; PMID:2897102
A:Accession: S00727

A:Molecule type: DNA
A:Residues: 1-545 <SCO>
A:Cross-references: UNIPROT:Q85468; UNIPROT:Q64895; UNIPARC:UPI000017561E; EMBL:X06943
C:Genetics:
A:Gene: erbB
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase
F:135-400/Domain: protein kinase homology <KIN>
F:143-151/Region: protein kinase ATP-binding motif

Query Match 85.4%; Score 35; DB 2; Length 545;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
|||||
Db 106 RLLOQERELV 114

RESULT 8
T46251
hypothetical protein DKFp761C241.1 - human
C:Species: Homo sapiens (man)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46251
R:Ottewaelde, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23031
A:Accession: T46251
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-565 <AAA>
A:Cross-references: UNIPROT:Q9HBM0; UNIPARC:UPI000002B6B9; EMBL:AL137497
A:Experimental source: adult amygdala; clone DKFp761C241
C:Genetics:
A>Note: DKFp761C241.1

Query Match 85.4%; Score 35; DB 2; Length 565;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
|||||
Db 175 RLLOQETELV 183

RESULT 9
TVU0H
protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H)
C:Species: avian erythroblastosis virus
C>Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 05-Oct-2004
C:Accession: A00644; A38022
R:Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.
Cell 35, 71-78, 1983
A>Title: The erbB gene of avian erythroblastosis virus is a member of the src gene fami
A:Reference number: A00644; MUID:84026539; PMID:6313229
A:Accession: A00644
A:Molecule type: DNA
A:Residues: 1-604 <YAM>
A:Cross-references: UNIPROT:P00535; UNIPARC:UPI000002BA64; GB:K01216; NID:9209676; PIDN
R:Debuire, B.; Henry, C.; Benaisa, M.; Biserre, G.; Claverie, J.M.; Saulle, S.; Martin,
Science 224, 1456-1459, 1984
A>Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of
A:Reference number: A38022; MUID:84223957; PMID:6328658
A:Accession: A38022
A:Molecule type: DNA
A:Residues: 1-28,'W',30-139,'F',141-145,'V',147-152 <DEB>
A:Cross-references: UNIPARC:UPI00001725C9; GB:K02006
C:Genetics:
A:Gene: erbB
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C:Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific
F:130-395/Domain: protein kinase homology <KIN>

F;138-146/Region: protein kinase ATP-binding motif
F;165/Active site: Lys #status predicted

Query Match 85.4%; Score 35; DB 1; Length 604;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8: Conservative 0; Mismatches 1: Indels

Qy 1 RLLQETELV 9
||| |
Db 101 RLLOERELV 109

RESULT 10
TVEFVLV

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus
N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
C;Species: avian leukosis virus, ALV
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004
C;Accession: B00643; A00643
R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.
Cell 41, 719-726, 1985
A;Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA processing and
A;Reference number: A00643; MUID:85228222; PMID:2988784
A;Accession: B00643
A;Molecule type: mRNA
A;Residues: 1-698 <NLI>
A;Cross-references: UNIPROT:P00534; UNIPARC:UPI00000171313; GB:M10066; GB:M13881; NID:Q211
A;Note: In Genbank entry CHKERBBF, release 109.0, the source is designated as Gallus gallus
C;Comment: This protein is synthesized as a gag-env-erbB protein.
C;Genetics:
A;Gene: gag-env-erbB
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific P
P;1-6/Product: gag protein (fragment) #status predicted <GAG>
P;7-59/Product: env protein (fragment) #status predicted <ENV>
P;60-698/Product: protein-tyrosine kinase erbB #status predicted <ERB>
P;194-459/Domain: protein kinase homology <KIN>
P;202-210/Region: protein kinase ATP-binding motif
P;229/Active site: Lys #status predicted

Query Match 85.4%; Score 35; DB 1; Length 698;
Best Local Similarity 88.9%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 1; Indels

QY 1 RLLQETELV 9
|||
165 RLLQETELV 173

RESULT 11
T33040
hypothetical protein T22B2.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 23-Oct-1999 #sequence_revision 29-Oct-1999 #tex-
C:Accession: T33040
R:Bentley, D.
submitted to the EMBL Data Library, February 1998
A:Description: The sequence of *C. elegans* cosmid T22B2.

Query Match 85.4% Score 35; DB 2; Length 955;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 0; Indels
Map position: X
Introns: 90/3; 172/3; 266/3; 670/2; 699/2; 727/2

QY 1 RLLQETELV 9
|||:||||:
765 PLLEETELI 773
DB

RESULT 12
GOHIE

CDate: 15-Nov-1984 #sequence revision 27-Nov-1985 #text change 05-Oct-2004
 CAccession: A00641; A25772; S30024; A36672; A43615; A23062; A05281; A33333; A33334; A33335; A33336; A33337; A33338; A33339; A33340; A33341; A33342; A33343; A33344; A33345; A33346; A33347; A33348; A33349; A33350; A33351; A33352; A33353; A33354; A33355; A33356; A33357; A33358; A33359; A33360; A33361; A33362; A33363; A33364; A33365; A33366; A33367; A33368; A33369; A33370; A33371; A33372; A33373; A33374; A33375; A33376; A33377; A33378; A33379; A33380; A33381; A33382; A33383; A33384; A33385; A33386; A33387; A33388; A33389; A33390; A33391; A33392; A33393; A33394; A33395; A33396; A33397; A33398; A33399; A33400; A33401; A33402; A33403; A33404; A33405; A33406; A33407; A33408; A33409; A33410; A33411; A33412; A33413; A33414; A33415; A33416; A33417; A33418; A33419; A33420; A33421; A33422; A33423; A33424; A33425; A33426; A33427; A33428; A33429; A33430; A33431; A33432; A33433; A33434; A33435; A33436; A33437; A33438; A33439; A33440; A33441; A33442; A33443; A33444; A33445; A33446; A33447; A33448; A33449; A33450; A33451; A33452; A33453; A33454; A33455; A33456; A33457; A33458; A33459; A33460; A33461; A33462; A33463; A33464; A33465; A33466; A33467; A33468; A33469; A33470; A33471; A33472; A33473; A33474; A33475; A33476; A33477; A33478; A33479; A33480; A33481; A33482; A33483; A33484; A33485; A33486; A33487; A33488; A33489; A33490; A33491; A33492; A33493; A33494; A33495; A33496; A33497; A33498; A33499; A33500; A33501; A33502; A33503; A33504; A33505; A33506; A33507; A33508; A33509; A33510; A33511; A33512; A33513; A33514; A33515; A33516; A33517; A33518; A33519; A33520; A33521; A33522; A33523; A33524; A33525; A33526; A33527; A33528; A33529; A33530; A33531; A33532; A33533; A33534; A33535; A33536; A33537; A33538; A33539; A33540; A33541; A33542; A33543; A33544; A33545; A33546; A33547; A33548; A33549; A33550; A33551; A33552; A33553; A33554; A33555; A33556; A33557; A33558; A33559; A33560; A33561; A33562; A33563; A33564; A33565; A33566; A33567; A33568; A33569; A33570; A33571; A33572; A33573; A33574; A33575; A33576; A33577; A33578; A33579; A33580; A33581; A33582; A33583; A33584; A33585; A33586; A33587; A33588; A33589; A33590; A33591; A33592; A33593; A33594; A33595; A33596; A33597; A33598; A33599; A33600; A33601; A33602; A33603; A33604; A33605; A33606; A33607; A33608; A33609; A33610; A33611; A33612; A33613; A33614; A33615; A33616; A33617; A33618; A33619; A33620; A33621; A33622; A33623; A33624; A33625; A33626; A33627; A33628; A33629; A33630; A33631; A33632; A33633; A33634; A33635; A33636; A33637; A33638; A33639; A33640; A33641; A33642; A33643; A33644; A33645; A33646; A33647; A33648; A33649; A33650; A33651; A33652; A33653; A33654; A33655; A33656; A33657; A33658; A33659; A33660; A33661; A33662; A33663; A33664; A33665; A33666; A33667; A33668; A33669; A33670; A33671; A33672; A33673; A33674; A33675; A33676; A33677; A33678; A33679; A33680; A33681; A33682; A33683; A33684; A33685; A33686; A33687; A33688; A33689; A33690; A33691; A33692; A33693; A33694; A33695; A33696; A33697; A33698; A33699; A33700; A33701; A33702; A33703; A33704; A33705; A33706; A33707; A33708; A33709; A33710; A33711; A33712; A33713; A33714; A33715; A33716; A33717; A33718; A33719; A33720; A33721; A33722; A33723; A33724; A33725; A33726; A33727; A33728; A33729; A33730; A33731; A33732; A33733; A33734; A33735; A33736; A33737; A33738; A33739; A33740; A33741; A33742; A33743; A33744; A33745; A33746; A33747; A33748; A33749; A33750; A33751; A33752; A33753; A33754; A33755; A33756; A33757; A33758; A33759; A33760; A33761; A33762; A33763; A33764; A33765; A33766; A33767; A33768; A33769; A33770; A33771; A33772; A33773; A33774; A33775; A33776; A33777; A33778; A33779; A33780; A33781; A33782; A33783; A33784; A33785; A33786; A33787; A33788; A33789; A33790; A33791; A33792; A33793; A33794; A33795; A33796; A33797; A33798; A33799; A33800; A33801; A33802; A33803; A33804; A33805; A33806; A33807; A33808; A33809; A33810; A33811; A33812; A33813; A33814; A33815; A33816; A33817; A33818; A33819; A33820; A33821; A33822; A33823; A33824; A33825; A33826; A33827; A33828; A33829; A33830; A33831; A33832; A33833; A33834; A33835; A33836; A33837; A33838; A33839; A33840; A33841; A33842; A33843; A33844; A33845; A33846; A33847; A33848; A33849; A33850; A33851; A33852; A33853; A33854; A33855; A33856; A33857; A33858; A33859; A33860; A33861; A33862; A33863; A33864; A33865; A33866; A33867; A33868; A33869; A33870; A33871; A33872; A33873; A33874; A33875; A33876; A33877; A33878; A33879; A33880; A33881; A33882; A33883; A33884; A33885; A33886; A33887; A33888; A33889; A33890; A33891; A33892; A33893; A33894; A33895; A33896; A33897; A33898; A33899; A33900; A33901; A33902; A33903; A3

A;Residues: 1028-1210 <SIM>
 A;Cross-references: UNIPARC:UPI00001725BF
 R;Weber, W.; Gill, G.N.; Speiss, J.
 Science 224, 294-297, 1984
 A;Reference number: A05281; MUID:84172183; PMID:6324343
 A;Accession: A05281
 A;Molecule type: protein
 A;Residues: 25-30, 'S', '32-51,454-467 <WEB>
 A;Cross-references: UNIPARC:UPI00001725C0; UNIPARC:UPI00001725C1
 R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.
 J. Biol. Chem. 260, 5205-5208, 1985
 A;Title: Identification of residues in the nucleotide binding site of the epidermal growth factor receptor
 A;Reference number: A60143; MUID:85182650; PMID:2395580
 A;Accession: A60143
 A;Molecule type: protein
 A;Residues: 740-744, 'X', '746-747 <RUS>
 A;Cross-references: UNIPARC:UPI00001725C2
 R;Mroczkowski, B.; Morig, G.; Cohen, S.
 Nature 309, 270-273, 1984
 A;Title: ATP-stimulated interaction between epidermal growth factor receptor and superoxide dismutase
 A;Reference number: A38023; MUID:84191554; PMID:6325948
 A;Contents: annotation; receptor activity
 A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
 R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.
 Cell 59, 33-43, 1989
 A;Title: Functional independence of the epidermal growth factor receptor from a domain x
 A;Reference number: A33331; MUID:90003233; PMID:2790960
 A;Contents: annotation; internalization signal
 C;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor
 C;Genetics:
 A;Gene: GDB:EGFR
 A;Cross-references: GDB:120610; OMIM:131550
 A;Map position: 7p12.3-7p12.1
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotyrosine
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-1210/Product: EGF receptor #status predicted <MAT>
 F;25-645/Domain: extracellular #status predicted <EXT>
 F;75-300/Domain: EGF receptor extracellular domain repeat <EE1>
 F;390-600/Domain: EGF receptor extracellular domain repeat <EE2>
 F;646-668/Domain: transmembrane #status predicted <TMW>
 F;669-1210/Domain: intracellular #status predicted <INT>
 F;710-975/Domain: protein kinase homology <KIN>
 F;718-726/Region: protein kinase ATP-binding motif
 F;999-1046/Region: coated-pit mediated internalization signal
 F;1047-1210/Region: inhibitory
 F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;745/Active site: Lys #status experimental

Query Match 85.4%; Score 35; DB 1; Length 1210;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
 Db 681 RLLOERELV 689
 ||||| |||

RESULT 13
 A53183
 epidermal growth factor receptor precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 05-Oct-2004
 A;Accession: A53183; A43818; S24942; A28941; S45325; I49643
 R;Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;
 Genes Dev. 8, 399-413, 1994
 A;Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor
 A;Reference number: A53183; MUID:94170986; PMID:8125255
 A;Accession: A53183
 A;Molecule type: mRNA
 A;Residues: 1-1210 <LUS>
 A;Cross-references: UNIPROT:Q01279; UNIPARC:UPI0000175614; GB:U03425
 R;Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.

Oncogene 6, 673-676, 1991
 A;Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site
 A;Reference number: A43818; MUID:91232866; PMID:2030916
 A;Accession: A43818
 A;Molecule type: mRNA
 A;Residues: 1-714 <AVI>
 A;Cross-references: UNIPARC:UPI0000175615; GB:X59698
 R;Bisinger, D.P.; Serrero, G.
 submitted to the EMBL Data Library, June 1992
 A;Reference number: S24942
 A;Accession: S24942
 A;Molecule type: mRNA
 A;Residues: 969-971, 'K', '973-1115, 'D' <BIS>
 A;Cross-references: UNIPARC:UPI0000175616; EMBL:Z12608
 R;Heisermann, G.J.; Gill, G.N.
 J. Biol. Chem. 263, 13152-13158, 1988
 A;Title: Epidermal growth factor receptor threonine and serine residues phosphorylated
 A;Reference number: A28941; MUID:88330814; PMID:3138233
 A;Accession: A28941
 A;Molecule type: protein
 A;Residues: 689-694, 'X', '696-704, 'L', '706-707;989-992, 'XX', '995-996, 'X', '998-1000;1002-1009
 A;Cross-references: UNIPARC:UPI0000175617; UNIPARC:UPI0000175618; UNIPARC:UPI0000175619
 R;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
 submitted to the EMBL Data Library, April 1994
 A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
 A;Reference number: S45325
 A;Accession: S45325
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-971, 'K', '973-1210 <VER>
 A;Cross-references: UNIPARC:UPI000002182B; EMBL:X78987; NID:G488830; PIDN:CAA55587.1; PID
 R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.
 Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993
 A;Title: Expression of the epidermal growth factor receptor gene is regulated in mouse
 A;Reference number: I49643; MUID:93126380; PMID:7678348
 A;Accession: I49643
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 12-20,22-132 <RES>
 A;Cross-references: UNIPARC:UPI000016CD26; GB:L06864; NID:gi93001; PIDN:AAAS3029.1; PID
 C;Genetics:
 A;Gene: EGFR
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphotyrosine
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;648-670/Domain: transmembrane #status predicted <TMW>
 F;712-977/Domain: protein kinase homology <KIN>
 F;720-728/Region: protein kinase ATP-binding motif
 F;680,695/Binding site: phosphate (Thr) (covalent) #status experimental
 F;697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
 F;993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
 F;1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
 F;1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 85.4%; Score 35; DB 2; Length 1210;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
 Db 683 RLLOERELV 691
 ||||| |||

RESULT 14
 TWCHLV
 epidermal growth factor receptor precursor - chicken
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
 C;Species: Gallus gallus (chicken)
 C;Date: 28-Feb-1986 #sequence revision 05-May-1995 #text change 05-Oct-2004
 R;Jax, I.; Johnson, A.; Hawk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Vennstr.
 Mol. Cell. Biol. 8, 1970-1978, 1988
 A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in mo

A;Reference number: A27720; MUID:88261272; PMID:3260329
 A;Accession: A27720
 A;Molecule type: mRNA
 A;Residues: 1-1223 <LAX>
 A;Cross-references: UNIPROT:P00534; UNIPARC:UPI00001725C3; GB:M20386
 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M. Cell 41, 719-726, 1985
 A;Title: C-erbB activation in ALV-induced erythroblastosis: novel RNA processing and product formation
 A;Reference number: A00643; MUID:85228222; PMID:2988784
 A;Accession: A00643
 A;Molecule type: mRNA
 A;Residues: 585-1223 <NIL>
 A;Cross-references: UNIPARC:UPI00001725C4; GB:M10066
 C;Genetics:
 A;Gene: erbB
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor specific protein kinase
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-1223/Product: epidermal growth factor receptor #status predicted <MAT>
 F;31-654/Domain: extracellular #status predicted <EXT>
 F;81-307/Domain: EGF receptor extracellular domain repeat <EE1>
 F;397-610/Domain: EGF receptor extracellular domain repeat <EE2>
 F;655-677/Domain: transmembrane #status predicted <TM>
 F;678-1223/Domain: intracellular #status predicted <INT>
 F;719-984/Domain: protein kinase homology <KIN>
 F;727-735/Region: protein kinase ATP-binding motif
 F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F;192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F;687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F;754/Active site: Lys #status predicted
 F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 85.4%; Score 35; DB 1; Length 1223;
 Best Local Similarity 88.9%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RLQETELV 9
 Db 690 RLQERELV 698

RESULT 15
 I52716
 Gene neu protein - hamster (fragment)
 C;Species: Cricetinae gen. sp. (hamster)
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Oct-2004
 C;Accession: I52716
 R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Nemoto, T.; Hara, M.; Ishikawa, T. Cancer Res. 54, 976-980, 1994
 A;Title: neu proto-oncogene mutation is specific for the neurofibromas in a N-nitroso-N-methyl-N'-nitro-N-nitrosoguanidine-induced rat neurofibrosarcoma
 A;Reference number: I52716; MUID:94147418; PMID:7906199
 A;Accession: I52716
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-46 <RES>
 A;Cross-references: UNIPARC:UPI0000086B07; GB:S69086; NID:G545490; PIDN:AAB29944.1; PID: I52716
 C;Genetics:
 A;Gene: neu
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
 C;Keywords: ATP

Query Match 80.5%; Score 33; DB 2; Length 46;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQETE 7
 Db 40 RLQETE 46

Search completed: March 1, 2006, 02:51:31
 Job time : 40 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 02:46:52 ; Search time 227 Seconds
(without alignments)
27.972 Million cell updates/sec

Title: US-09-583-200F-22

Perfect score: 41

Sequence: 1 RLQETELV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	36	Q9NP09 HUMAN	Q9NP09 homo sapien
2	41	100.0	304	Q68KJ7 FELCA	Q68KJ7 felis silve
3	41	100.0	435	Q6ZNM4 HUMAN	Q6ZNM4 homo sapien
4	41	100.0	881	Q8COE7 MOUSE	Q8COE7 m mus muscu
5	41	100.0	1254	1 ERBB2_MOUSE	Q60553 mesocricetu
6	41	100.0	1255	1 ERBB2_HUMAN	P04626 homo sapien
7	41	100.0	1257	1 ERBB2_RAT	P06494 rattus norv
8	41	100.0	1259	1 ERBB2_CANFA	O18735 canis fami
9	41	100.0	1259	2 Q8K3F9 RAT	Q8K3F9 rattus norv
10	41	100.0	1305	2 Q6ZPE0 MOUSE	Q6ZPE0 mus musculu
11	35	85.4	202	2 Q6QT04 CANFA	Q6QT04 canis fami
12	35	85.4	276	2 Q8BYH4 MOUSE	Q8BYH4 mus musculu
13	35	85.4	540	1 ERBB_AVIEU	P11273 avian eryth
14	35	85.4	545	2 Q85468 9RETR	Q85468 avian eryth
15	35	85.4	567	2 Q86714_AVEVR	Q86714 avian rous-
16	35	85.4	604	1 ERBB_AVIER	P00535 avian eryth
17	35	85.4	634	1 ERBB_ALV	P00534 avian leuko
18	35	85.4	639	2 Q8BYI2 MOUSE	Q8BYI2 mus musculu
19	35	85.4	703	1 EGFR_CHICK	P13387 gallus gall
20	35	85.4	729	2 Q86712_AVEVR	Q86712 avian rous-
21	35	85.4	731	2 Q6PIQ3_HUMAN	Q6PIQ3 homo sapien
22	35	85.4	731	2 Q5REL7_PONPY	Q5REL7 pongo pygma
23	35	85.4	774	2 Q6PCG6_XENLA	Q6PCG6 xenopus lae
24	35	85.4	779	1 VEZA_HUMAN	Q9HBM0 homo sapien
25	35	85.4	780	2 Q8BZB5 MOUSE	Q8BZB5 mus musculu
26	35	85.4	782	2 Q5XI52_RAT	Q5XI52 rattus norv
27	35	85.4	955	2 Q45195_CABEL	Q45195 caenorhabdi
28	35	85.4	962	2 Q64895 9RETR	Q64895 avian eryth
29	35	85.4	1081	2 Q59FL8_HUMAN	Q59FL8 homo sapien
30	35	85.4	1091	2 Q504U8_HUMAN	Q504U8 homo sapien
31	35	85.4	1094	2 Q4RWY4_TETNG	Q4RWY4 tetraodon n

32	35	85.4	1165	2 Q9YH40_XIPXI	Q9YH40 xiphophorus
33	35	85.4	1191	2 Q6VQA3_BRARE	Q6VQA3 brachydanio
34	35	85.4	1191	2 Q7SZF7_BRARE	Q7SZF7 brachydanio
35	35	85.4	1209	2 Q8MIL8_PIG	Q8MIL8 sus scrofa
36	35	85.4	1209	2 Q9OX70_RAT	Q9OX70 rattus norv
37	35	85.4	1210	1 EGFR_HUMAN	P00533 homo sapien
38	35	85.4	1210	1 EGFR_MOUSE	Q01279 mus musculu
39	35	85.4	1210	2 Q9EP98 MOUSE	Q9EP98 mus musculu
40	35	85.4	1210	2 Q5SVB8 MOUSE	Q5SVB8 mus musculu
41	34	82.9	711	2 Q80Y89_MOUSE	Q80Y89 mus musculu
42	34	82.9	846	2 Q4S5A9_TETNG	Q4S5A9 tetraodon n
43	33	80.5	46	2 Q6394C_9RODE	Q63946 cricetinae
44	33	80.5	272	2 Q85Z26_MUSDU	Q85Z26 mus dummi
45	33	80.5	272	2 Q860A1_9MURI	Q860A1 mus abbotti

ALIGNMENTS

RESULT 1
Q9NP09 HUMAN
ID Q9NP09 HUMAN PRELIMINARY; PRT; 36 AA.
AC Q9NP09
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ERBB2 (Fragment).
GN Name=ERBB2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=94169396; PubMed=7907235;
RA Briscoe W.T., Ray D.B., Airhart J.L., Ratliff A.L., Shockley E.A.,
RA Whetsell L., Schaefer F.V., Williams R.M.;
RT "A new high frequency polymorphism in the HER-2/neu oncogene in normal
RT tissue and breast tumors."
RL Breast Cancer Res. Treat. 28:45-49(1993).
DR EMBL; M86910; AAF30295.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 36
SQ SEQUENCE 36 AA; 4204 MW; 230DA20B669F67D5 CRC64;

Query Match 100.0%; Score 41; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
DB 6 RLQETELV 14

RESULT 2
Q68KJ7 FELCA
ID Q68KJ7 FELCA PRELIMINARY; PRT; 304 AA.
AC Q68KJ7;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE HER2 (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15705889;
RA De Maria R., Olivero M., Iussich S., Nakaichi M., Murata T.,

RA Biolatti B., Di Renzo M.F.;
 RT "Spontaneous Peline Mammary Carcinoma Is a Model of HER2
 RT Overexpressing Poor Prognosis Human Breast Cancer.";
 RL Cancer Res. 65:907-912(2005).
 DR ENBL, AY685128; AAU01910.1; -, Genomic_DNA.
 DR SMR, Q68KJ7; 57-304.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PR0109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Transferase.
 FT NON_TER 1 1
 FT NON_TER 304 304
 SQ SEQUENCE 304 AA; 33934 MW; 47C0290F4BC020ED CRC64;
 Query Match 100.0%; Score 41; DB 2; Length 304;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLQETELV 9
 DB 42 RLQETELV 50
 RESULT 3
 Q6ZMM4 HUMAN
 ID Q6ZMM4_HUMAN PRELIMINARY; PRT; 435 AA.
 AC Q6ZMM4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein FLJ16821.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Trachea;
 RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
 RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wazutsuuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahashi K., Masuho Y., Nagai K., Isegai T.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AK131568; BAD18701.1; -, mRNA.
 DR SMR, Q6ZMM4; 254-434.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001450; 4FeS_ferredoxin.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000719; Prot_Kinase.

DR InterPro; IPR002290; Ser thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR PRINTS; PR00333; 4FE4SFRDXXIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 2.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Kinase; Receptor; Tyrosine-protein kinase.
 SQ SEQUENCE 435 AA; 47891 MW; 1FA846710D31311A CRC64;
 Query Match 100.0%; Score 41; DB 2; Length 435;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLQETELV 9
 DB 239 RLQETELV 247
 RESULT 4
 Q8COE7 MOUSE
 ID Q8COE7_MOUSE PRELIMINARY; PRT; 881 AA.
 AC Q8COE7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
 DE enriched library, clone:6030449F08 product:v-erb-b2 erythroblastic
 DE leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene
 DE homolog (avian), full insert sequence. (Fragment).
 GN Name=ErbB2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleisichmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyehaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Kato H., Kawai J., Kojima Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Segabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK031542; BAC27442.1; -; mRNA.
 DR HSSP; P06494; IN8Y.
 DR SMR; P06494; IN8Y.
 DR SMR; Q8C0E7; 1-255.
 DR Ensembl; ENSMUSG00000062312; Mus musculus.
 DR MGI; MGI:95410; Erbb2.
 DR GO; GO:0016324; C:apical plasma membrane; IDA.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007507; P:heart development; IMP.
 DR GO; GO:0042552; P:myelination; IMP.
 DR GO; GO:0007422; P:peripheral nervous system development; IMP.
 DR InterPro; IPR000494; EGFR_L.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR InterPro; IPR008266; Tyr_Pkinase_AS.
 DR Pfam; PF01030; Recep_L_domain; 1.
 DR Pfam; PF02757; YLP; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 2.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Transferase;
 TYROSINE-protein kinase.
 FT NON_1 1

SQ SEQUENCE 881 AA; 97501 MW; 5D5042BB9F8F0836 CRC64;
 Query Match 100.0%; Score 41; DB 2; Length 881;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLQSTELV 9
 Db 315 RLQSTELV 323
 RESULT 5
 ERBB2_MESAU
 ID ERBB2_MESAU STANDARD; PRT; 1254 AA.
 AC Q60553;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
 GN Name=ERBB2; (C-erbB-2) (NEU proto-oncogene).
 GN Name=ERBB2; Synonym=NEU;
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Cricetidae; Cricetinae; Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Nerve;
 RX MEDLINE=94193007; PubMed=7908275; DOI=10.1016/0378-1119(94)90553-3;
 RA Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M., Yamazaki Y.,
 RA Ishikawa T.;
 RL Gene 140:251-255(1994).
 CC "Cloning and activation of the Syrian hamster neu proto-oncogene.";
 CC -!- FUNCTION: Essential component of a neurotrophin-receptor complex,
 CC although neurotrophins do not interact with it alone. GP30 is a
 CC potential ligand for this receptor. Not activated by EGF, TGF-
 CC alpha and amphiregulin (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
 CC (Potential). Part of a complex with EGFR and either PIK3C2A or
 CC PIK3C2B. Interacts with PRKCAP and PLXNB1. May interact with
 CC PIK3CB. When phosphorylated on Tyr-1196 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine
 CC residues.
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
 CC subfamily.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; D16295; BAA03801.1; -; mRNA.
 DR PIR; I48161; I48161.
 DR HSSP; P06494; IN8Y.
 DR SMR; Q60553; 23-629.
 DR InterPro; IPR000494; EGFR_L.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR InterPro; IPR008266; Tyr_Pkinase_AS.
 DR InterPro; IPR004019; YLP motif.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR Pfam; PF02757; YLP; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 4.

DR SMART: SM00219; TykC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 KW ATP-binding; Disease mutation; Glycoprotein; Kinase; Multigene family;
 KW Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
 KW Transferase; Transmembrane; Tyrosine-protein kinase.
 PT SIGNAL 1 21 Potential.
 FT CHAIN 22 1254 Receptor tyrosine-protein kinase erbB-2.
 FT TOPO_DOM 22 652 Extracellular (Potential).
 FT TRANSMEM 653 675 Potential.
 FT TOPO_DOM 676 1254 Cytoplasmic (Potential).
 FT DOMAIN 720 987 Protein kinase.
 FT NP_BIND 726 734 ATP (By similarity).
 FT REGION 1195 1197 Interaction with PIK3C2B (By similarity).
 FT COMPTAS 158 368 Cys-rich.
 FT COMPTAS 472 644 Cys-rich.
 FT ACT_SITE 845 845 ATP (By similarity).
 FT BINDING 753 753 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 1139 1139 similarity).
 FT MOD_RES 1196 1196 Phosphotyrosine (Potential).
 FT MOD_RES 1247 1247 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 187 187 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 530 530 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 571 571 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 629 629 N-linked (GlcNAc...) (Potential).
 FT DISULFID 195 202 By similarity.
 FT DISULFID 199 212 By similarity.
 FT DISULFID 236 244 By similarity.
 FT DISULFID 240 252 By similarity.
 FT DISULFID 255 264 By similarity.
 FT DISULFID 268 295 By similarity.
 FT DISULFID 299 311 By similarity.
 FT DISULFID 315 331 By similarity.
 FT DISULFID 334 338 By similarity.
 FT DISULFID 511 520 By similarity.
 FT DISULFID 515 528 By similarity.
 FT DISULFID 531 540 By similarity.
 FT DISULFID 544 560 By similarity.
 FT DISULFID 563 576 By similarity.
 FT DISULFID 567 584 By similarity.
 FT DISULFID 587 596 By similarity.
 FT DISULFID 600 623 By similarity.
 FT DISULFID 626 634 By similarity.
 FT DISULFID 630 642 By similarity.
 FT VARIANT 658 658 V -> E (in oncogenic NEU).
 FT VARIANT 659 659 V -> E (in oncogenic NEU).
 SQ SEQUENCE 1254 AA; 138253 MW; 974C3791C21F2BE1 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQETELV 9
 |||||
 Db 689 RLQETELV 697

RESULT 6
 ERBB2_HUMAN
 ID ERBB2_HUMAN STANDARD; PRT; 1255 AA.
 AC P04626; O61DVI; OSUMK4;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
 DE (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Tyrosine kinase-type cell
 DE surface receptor HER2) (MLN 19).

GN Name=ERBB2; Synonyms=HER2, NEU, NGL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86118663; PubMed=3003577;
 RA Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
 RA Saito T., Toyoshima K.;
 RT "Similarity of protein encoded by the human c-erb-B-2 gene to
 RT epidermal growth factor receptor.";
 RL Nature 319:230-234(1986).
 RN [2]
 RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-1170.
 RX MEDLINE=86070181; PubMed=2999974;
 RA Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., McGrath J.,
 RA Seeburg P.H., Libermann T.A., Schlessinger J., Franke U.,
 RA Levinson A., Ullrich A.;
 RT "Tyrosine kinase receptor with extensive homology to EGF receptor
 RT shares chromosomal location with neu oncogene.";
 RL Science 230:1132-1139(1985).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-452; VAL-655 AND
 RP ALA-1170.
 RA Bieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
 RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE OF 1-191.
 RX MEDLINE=87286898; PubMed=3039351;
 RA Tal M., King C.R., Kraus M.H., Ullrich A., Schlessinger J., Givol D.;
 RT "Human HER2 (neu) promoter: evidence for multiple mechanisms for
 RT transcriptional initiation.";
 RL Mol. Cell. Biol. 7:2597-2601(1987).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 737-1031.
 RX MEDLINE=86016729; PubMed=2995967;
 RA Semba K., Kamata N., Toyoshima K., Yamamoto T.;
 RT "A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-
 RT erbB-1/epidermal growth factor-receptor gene and is amplified in a
 RT human salivary gland adenocarcinoma.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).
 RN [6]
 RP NUCLEOTIDE SEQUENCE OF 832-909.
 RC TISSUE=Mammary carcinoma;
 RX MEDLINE=85272597; PubMed=2992089;
 RA King C.R., Kraus M.H., Aaronson S.A.;
 RT "Amplification of a novel v-erbB-related gene in a human mammary
 RT carcinoma.";
 RL Science 229:974-976(1985).
 RN [7]
 RP NUCLEOTIDE SEQUENCE OF 1081-1245, AND VARIANT ALA-1170.
 RX MEDLINE=94000386; PubMed=8104414;
 RA Sarkar F.H., Ball D.E., Li Y.W., Crissman J.D.;
 RT "Molecular cloning and sequencing of an intron of Her-2/neu (ERBB2)
 RT gene.";
 RL DNA Cell Biol. 12:611-615(1993).
 RN [8]
 RP IDENTIFICATION IN A COMPLEX WITH PIK3C2A AND EGFR, IDENTIFICATION IN A
 RP COMPLEX WITH PIK3C2B AND EGFR, AND INTERACTION WITH PIK3C2B.
 RX PubMed=10805725;
 RA Arcaro A., Zvelebil M.J., Wallasch C., Ullrich A., Waterfield M.D.,
 RA Domin J.;
 RT "Class II phosphoinositide 3-kinases are downstream targets of
 RT activated polypeptide growth factor receptors.";
 RL Mol. Cell. Biol. 20:3817-3830(2000).
 RN [9]
 RP INTERACTION WITH PLXNB1.

RX PubMed=15210733; DOI=10.1083/jcb.200312094;
RA Swiercz J.M., Kuner R., Offermanns S.;
RT Plexin-B1/RhoGTP-mediated RhoA activation involves the receptor
RT tyrosine kinase ErbB-2.;
RL J. Cell Biol. 165:869-880(2004).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 654-662 IN COMPLEX WITH HLA
RP AND BETA-2 MICROGLOBULIN.
RX MEDLINE=2062861; PubMed=1059398; DOI=10.1074/jbc.274.51.36422;
RA Kuhns J.J., Batalia M.A., Yan S., Collins E.J.;
RT "Poor binding of a HER-2/neu epitope (GP2) to HLA-A2.1 is due to a
RT lack of interactions with the center of the peptide";
RL J. Biol. Chem. 274:36422-36427(1999).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.52 ANGSTROMS) OF 23-629 IN COMPLEX WITH FAB.
RX MEDLINE=22497871; PubMed=12610629; DOI=10.1038/nature01392;
RA Cho H.-S., Mason K., Ramvar K.X., Stanley A.M., Gabelli S.B.,
RA Denney D.W. Jr., Leahy D.J.;
RT "Structure of the extracellular region of HER2 alone and in complex
RT with the Herceptin Fab.";
RL Nature 421:756-760(2003).
RN [12]
RP VARIANTS VAL-654 AND VAL-655.
RX MEDLINE=93194196; PubMed=8095488;
RA Ehsani A., Low J., Wallace R.B., Wu A.M.;
RT "Characterization of a new allele of the human ERBB2 gene by allele-
RT specific competition hybridization.";
RL Genomics 15:426-429(1993).
CC -!- FUNCTION: Essential component of a neuroligin-receptor complex,
CC although neuroligins do not interact with it alone. GP30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC (potential). Interacts with PRKCAP (by similarity). Binds PLXNB1.
CC Part of a complex with EGFR and either PIK3C2A or PIK3C2B. May
CC interact with PIK3C2B when phosphorylated on Tyr-1196.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC (by similarity).
CC -!- POLYMORPHISM: There are four alleles due to the variations in
CC positions 654 and 655. Allele B1 (ile-654/ile-655) has a frequency
CC of 0.782; allele B2 (ile-654/Val-655) has a frequency of 0.206;
CC allele B3 (Val-654/Val-655) has a frequency of 0.012.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; M11767; AAA35808.1; -; Genomic DNA.
DR EMBL; M11761; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11762; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11763; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11764; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11765; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11766; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11730; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M12036; AAA35978.1; -; mRNA.
DR EMBL; AY208911; CAA21082.1; -; Genomic DNA.
DR EMBL; X03363; CAA27060.1; -; mRNA.
DR EMBL; M16792; AAA58637.1; -; Genomic DNA.
DR EMBL; M16789; AAA58637.1; JOINED; Genomic DNA.
DR EMBL; M16790; AAA58637.1; JOINED; Genomic DNA.
DR EMBL; M16791; AAA58637.1; JOINED; Genomic DNA.
DR EMBL; L29395; AAA35809.1; -; Genomic DNA.
DR EMBL; M95667; AAC37531.1; -; Unassigned DNA.
DR PIR; A24571; A24571.
DR PDB; 1N8Z; X-ray; C=23-629.

DR PDB; 1OVC; Model; A=737-1031.
DR PDB; 1S78; X-ray; A/B=23-646.
DR Ensemble; ENSG00000141736; Homo sapiens.
DR HGNC; HGNC:3430; ERBB2.
DR MIM; 164870; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0005006; F:epidermal growth factor receptor activity; NAS.
DR GO; GO:0043125; F:Erbb-3 class receptor binding; TAS.
DR GO; GO:0046982; F:protein heterodimerization activity; NAS.
DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . ; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007507; P:heart development; TAS.
DR GO; GO:0030879; P:mammary gland development; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR GO; GO:0048015; P:phosphoinositide-mediated signaling; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0045765; P:regulation of angiogenesis; NAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; NAS.
DR InterPro; IPR00494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR001245; Tyr_Kinase.
DR InterPro; IPR008266; Tyr_Pkinase_AS.
DR InterPro; IPR004019; YLP motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW 3D-structure; ATP-binding; Glycoprotein; Kinase; Multigene family;
KW Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Signal;
KW Transference; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 21
FT CHAIN 22 1255 Receptor tyrosine-protein kinase erbB-2.
FT TOPO_DOM 22 552 Extracellular (Potential).
FT TRANSMEM 653 675 Potential.
FT TOPO_DOM 676 1255 Cytoplasmic (Potential).
FT DOMAIN 720 987 Protein kinase.
FT NP_BIND 756 734 ATP (By similarity).

Query Match 100.0%; Score 41; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQSTELV 9
|||
Db 689 RLQSTELV 697

RESULT 7
ERBB2 RAT STANDARD; PRT; 1257 AA.
ID ERBB2 RAT
AC P06494; Q8P732;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Epidermal growth factor
DE receptor-related protein).
DE Name=Erbb2; Synonyms=Neu;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Neuroblastoma;
RX MEDLINE=86118682; PubMed=3945311;
RA Bargmann C.I., Hung M.-C., Weinberg R.A.;
RT "The neu oncogene encodes an epidermal growth factor receptor-related
RT protein."
RL Nature 319:226-230(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Prostate;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 634-699.
RX MEDLINE=92035293; PubMed=1682063;
RA Masui T., Mann A.M., Macatee T.D., Garland E.M., Okamura T.,
RA Smith R.A., Cohen S.M.;
RT "Direct DNA sequencing of the rat neu oncogene transmembrane domain
RT reveals no mutation in urinary bladder carcinomas induced by N-butyl-
RT N-(4-hydroxybutyl)nitrosamine, N-[4-(5-nitro-2-furyl)-2-
RT thiazolyl]formamide or N-methyl-N-nitrosourea."
RL Carcinogenesis 12:1975-1978(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 852-905.
RC TISSUE=Sciatic nerve;
RX MEDLINE=91222560; PubMed=2025425; DOI=10.1016/0896-6273(91)90167-X;
RA Lai C., Lemke G.;
RT "An extended family of protein-tyrosine kinase genes differentially
RT expressed in the vertebrate nervous system."
RL Neuron 6:691-704(1991).
RN [5]
RP STRUCTURE BY NMR OF 650-668.
RX MEDLINE=92155181; PubMed=1346763;
RA Gullick W.J., Bottomley A.C., Lofts P.J., Doak D.G., Mulvey D.,
RA Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
RT "Three dimensional structure of the transmembrane region of the proto-
RT oncogenic and oncogenic forms of the neu protein."
RL EMBO J. 11:43-48(1992).
CC -1- FUNCTION: Essential component of a neurotrophin-receptor complex,
CC although neurotrophins do not interact with it alone. GP30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors. The
CC constitutively activated oncogenic variant forms a homodimer.
CC Interacts with PRKCAP and PLXNB1. Part of a complex with EGFR and
CC either PIK3C2A or PIK3C2B. May interact with PIK3C2B when
CC phosphorylated on Tyr-1198 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X03362; CAA27059.1; ALT INIT; mRNA.
CC EMBL; BC061863; AAH61863.1; ALT INIT; mRNA.
CC PIR; A24562; TVRTNU.
CC PDB; 1N8Y; X-ray; C=23-631.
CC DR Ensembl; ENSRNOG0000006450; Rattus norvegicus.
CC RGD; 2561; Erbb2.
CC GO; GO:004595; P:regulation of cell differentiation; TAS.
CC GO; GO:0042127; P:regulation of cell proliferation; TAS.
CC InterPro; IPR000494; EGFR_L.
CC InterPro; IPR006211; Furin-like.
CC InterPro; IPR006212; Furin repeat.
CC InterPro; IPR000719; Prot_Kinase.

DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 4.
DR SMART; SM00219; TyrcG; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW 3D-structure; ATP-binding; Disease mutation; Glycoprotein; Kinase;
KW Multigene family; Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW Receptor; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 1257 Receptor tyrosine-protein kinase erbB-2.
FT TOPO_DOM 22 654 Extracellular (Potential).
FT TRANSMEM 655 677 Potential.
FT TOPO_DOM 678 1257 Cytoplasmic (Potential).
FT DOMAIN 722 989 Protein kinase.
FT NP_BIND 728 736 ATP (By similarity).
FT REGION 1197 1199 Interaction with PIK3C2B (By similarity).
FT COMPBIAS 159 369 Cys-rich.
FT COMPBIAS 473 646 Cys-rich.
FT ACT_SITE 847 847 By similarity.
FT BINDING 755 755 ATP (By similarity).
FT MOD_RES 1141 1141 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT MOD_RES 1198 1198 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT MOD_RES 1250 1250 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 188 188 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 260 260 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 532 532 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 573 573 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 631 631 N-linked (GlcNAc...) (Potential).
FT DISULFID 196 205 By similarity.
FT DISULFID 220 213 By similarity.
FT DISULFID 221 228 By similarity.
FT DISULFID 225 236 By similarity.
FT DISULFID 237 245 By similarity.
FT DISULFID 241 253 By similarity.
FT DISULFID 256 285 By similarity.
FT DISULFID 269 296 By similarity.
FT DISULFID 300 312 By similarity.
FT DISULFID 316 332 By similarity.
FT DISULFID 335 339 By similarity.
FT DISULFID 513 522 By similarity.
FT DISULFID 517 530 By similarity.
FT DISULFID 533 542 By similarity.
FT DISULFID 546 562 By similarity.
FT DISULFID 565 578 By similarity.
FT DISULFID 569 586 By similarity.
FT DISULFID 589 598 By similarity.
FT DISULFID 602 625 By similarity.
FT DISULFID 628 636 By similarity.
FT DISULFID 632 644 By similarity.
FT VARIANT 661 661 V -> E (in oncogenic NEU).
FT CONFLICT 145 145 S -> G (in Ref. 2).
FT CONFLICT 505 509 LCVSS -> CGLE (in Ref. 2).
SQ SEQUENCE 1257 AA; 138832 MW; 6129264583011402 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQSTELV 9
|||
DB 691 RLQSTELV 699

RESULT 8
 ERBB2_CANFA STANDARD; PRT; 1259 AA.
 AC O18735;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
 DE (p185erbB2) (C-erbB-2).
 OS Name=ERBB2;
 GN Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RC TISSUE=Mammary gland;
 RA Yokota H.;
 RT "cDNA cloning of erbB-2 from canine mammary gland.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Essential component of a neuroligin-receptor complex,
 CC allthought neuregulins do not interact with it alone. GP30 is a
 CC potential ligand for this receptor. Not activated by EGF, TGF-
 CC alpha and amphiregulin (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
 CC (Potential). Interacts with PRKCAP. Binds PLXNB1. Part of a
 CC complex with EGFR and either PIK3C2A or PIK3C2B. May interact with
 CC PIK3C2B when phosphorylated on Tyr-1200 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
 CC (By similarity).
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
 CC subfamily.
 CC
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AB008451; BAA3127.1; -; mRNA.
 CC HSP; P04626; I88Z.
 CC SMR; O18735; 23-628.
 CC Ensembl; ENSCARG0000016351; Canis familiaris.
 CC InterPro; IPR000494; EGFR_L.
 CC InterPro; IPR006211; Furin-like.
 CC InterPro; IPR006212; Furin repeat.
 CC InterPro; IPR000719; Prot Kinase.
 CC InterPro; IPR001245; Tyr_kinase_AS.
 CC InterPro; IPR008266; Tyr_kinase.
 CC InterPro; IPR004019; YLP motif.
 CC Pfam; PF00757; Furin-like; 1.
 CC Pfam; PF01030; Recep_L domain; 2.
 CC Pfam; PF02757; YLP_2.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD0000001; Prot_kinase; 1.
 CC SMART; SM00261; FU; 3.
 CC SMART; SM00219; Tyrc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC ATP-binding; Glycoprotein; Kinase; Multigene family;
 CC Nucleotide-binding; Phosphorylation; Receptor; Signal; Transferase;
 CC Transmembrane; Tyrosine-protein kinase.
 CC SIGNAL 1 22 Potential.
 CC CHAIN 23 1259 Receptor tyrosine-protein kinase erbB-2.
 CC TOPO_DOM 23 653 Extracellular (Potential).
 CC TRANSMEM 654 674 Potential.
 CC TOPO_DOM 675 1259 Cytoplasmic (Potential).

FT DOMAIN 719 986 Protein kinase.
 FT NP_BIND 725 733 ATP (By similarity).
 FT REGION 1199 1201 Interaction with PIK3C2B (By similarity).
 FT COMPBIAS 192 268 Cys-rich.
 FT COMPBIAS 1101 1219 Pro-rich.
 FT ACT_SITE 844 844 By similarity.
 FT BINDING 752 752 ATP (By similarity).
 FT MOD_RES 1138 1138 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT MOD_RES 1200 1200 Phosphotyrosine (Potential).
 FT MOD_RES 1252 1252 Phosphotyrosine (by autocatalysis) (By
 FT similarity).
 FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 421 421 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 570 570 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc...) (Potential).
 FT DISULFID 195 204 By similarity.
 FT DISULFID 199 212 By similarity.
 FT DISULFID 220 227 By similarity.
 FT DISULFID 224 235 By similarity.
 FT DISULFID 236 244 By similarity.
 FT DISULFID 240 252 By similarity.
 FT DISULFID 255 264 By similarity.
 FT DISULFID 268 295 By similarity.
 FT DISULFID 299 311 By similarity.
 FT DISULFID 315 331 By similarity.
 FT DISULFID 334 338 By similarity.
 FT DISULFID 511 519 By similarity.
 FT DISULFID 514 527 By similarity.
 FT DISULFID 530 539 By similarity.
 FT DISULFID 543 559 By similarity.
 FT DISULFID 562 575 By similarity.
 FT DISULFID 566 583 By similarity.
 FT DISULFID 586 595 By similarity.
 FT DISULFID 599 622 By similarity.
 FT DISULFID 629 641 By similarity.
 FT DISULFID 629 641 By similarity.
 SQ SEQUENCE 1259 AA; 137991 MW; E37364D49C4ACD46 CRC64;
 Query Match 100.0%; Score 41; DB 1; Length 1259;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLQETELV 9
 DB 688 RLQETELV 696
 RESULT 9
 ID Q8K3F9_RAT PRELIMINARY; PRT; 1259 AA.
 AC Q8K3F9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Neu protooncoprotein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE_SEQUENCE.
 RC STRAIN=BDIX;
 RA Watson P.A., Kim K., Chen K.-S., Gould M.N.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DE EMBL; AY116182; AAM50093.1; -; mRNA.
 DR HSP; P06494; I88Z.
 DR SMR; Q8K3F9; 26-633.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.

DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	InterPro; IPR001245; Tyr_pkinase.
DR	InterPro; IPR008266; Tyr_pkinase_AS.
DR	InterPro; IPR004019; YLP_motif.
DR	Pfam; PF00757; Furin-like; 1.
DR	Pfam; PF01030; Recep_L_domain; 2.
DR	Pfam; PF02757; YLP_2_domain; 2.
DR	PRINTS; PR00109; TYRKINASE.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SM00261; FU; 4.
DR	SMART; SM00220; S_TKC; 1.
DR	SMART; SM00219; TYRK; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR	ATP-binding; Kinase; Nucleotide-binding; Transferase.
KW	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 1305 AA; 143508 MW; A51D897408521860 CRC64;
Query Match 100.0%; Score 41; DB 2; Length 1305;	
Best Local Similarity 100.0%; Pred.No.19;	
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 RLQETELV 9
Db	
	739 RLQETELV 747
RESULT 11	
Q6QT04	CANFA
ID	Q6QT04_CANFA PRELIMINARY; PRT; 202 AA.
AC	Q6QT04;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Epidermal growth factor receptor (Fragment).
GN	Name=EGFR;
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC	Canis.
EN	NCBI_TaxID=9615;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Dickinson P.J., Roberts B.N., Mallen-StClair J., Leutenegger C.M.,
RA	LeCouteur R.A.;
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY527212; AAS17990.1; -; mRNA.
DR	SNR; Q6QT04; 85-202.
DR	Ensembl; ENSCAFG0000003465; Canis familiaris.
DR	GO; GO:0005324; F:ATP binding; IEA.
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR000719; Prot_kinase.
DR	InterPro; IPR001245; Tyr_pkinase.
DR	ProDom; PD000001; Prot_kinase; 1.
DR	SMART; SM00219; TYRK; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
KW	ATP-binding; Nucleotide-binding; Receptor.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 202 AA; 22140 MW; 4CCBCD0514FFBEE CRC64;
Query Match 85.4%; Score 35; DB 2; Length 202;	
Best Local Similarity 88.9%; Pred.No.50;	
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 RLQETELV 9
Db	
	70 RLQETELV 78

RESULT 12
Q8BYB4 MOUSE
ID Q8BYB4 MOUSE PRELIMINARY; PRT; 276 AA.
AC Q8BYB4;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630004L17 product:TRANSMEMBRANE PROTEIN VEZATIN
DE homolog.
GN Name-AI854408;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai N., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK041354; BAC30915.1; -; mRNA.
DR MGI; MGI-2143698; A1854408.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
SQ SEQUENCE 276 AA; 31712 MW; 18E37DBFA6B246E7 CRC64;
Query Match 85.4%; Score 35; DB 2; Length 276;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLQETELV 9
DB 223 RLQETELV 231
RESULT 13
ID ERBB AVIEU STANDARD; PRT; 540 AA.
AC P11273;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
GN Name=V-ERBB;
OS Avian erythroblastosis virus (strain ts167).
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus.
OX NCBI_TaxID=103898;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=87064458; PubMed=2878364;
RA Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
RT "A single amino acid substitution in v-erbB confers a thermolabile
RT phenotype to ts167 avian erythroblastosis virus-transformed erythroid
RT cells.";
RL Mol. Cell. Biol. 6:1751-1759(1986).
CC -| CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -| SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
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CC removed.
CC EMBL; M13179; AAA42401.1; -; Genomic_RNA.
DR PIR; A25231; TVFVEB.
DR HSP; Q9H2C9; 1M17.
DR SMR; P11273; 116-439.
DR InterPro; IPR000719; Prot_kinase.

DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR008266; Tyr_pkinase_AS.
DR PRINTS; PD000001; Prot kinase; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Phosphorylation;
KW Transferase; Tyrosine-protein kinase.
FT DOMAIN 132 399 protein kinase.
FT NP_BIND 138 146 ATP (By similarity).
FT ACT_SITE 257 257 By similarity.
FT BINDING 165 165 ATP (By similarity).
FT VARIANT 270 270 H -> D (in thermolabile v-erbB).
SQ SEQUENCE 540 AA; 60413 MW; 5B53297AA068B65D CRC64;

Query Match 85.4%; Score 35; DB 1; Length 540;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLQETELV 9
DB 101 RLQERELV 109
|||||

RESULT 14
Q85468_9RETR PRELIMINARY; PRT; 545 AA.
AC Q85468;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE (ts34) v-erbB gene (Fragment).
OS Avian erythroblastosis virus.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus.
OX NCBI_TaxID=11861;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88217326; PubMed=2897102;
RA Bruekin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
RX Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
RT "six amino acids from the retroviral gene gag greatly enhance the
RT "Common site of mutation in the erbB gene of avian erythroblastosis
RT virus mutants that are temperature sensitive for transformation.";
RL Oncogene Res. 1:263-278(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9026603; PubMed=1969616;
RA Bruekin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
RT "six amino acids from the retroviral gene gag greatly enhance the
RT transforming potential of the oncogene v-erb-B.";
RL Oncogene 5:15-24(1990).
DR EMBL; X06943; CAA30024.1; -; Genomic_DNA.
DR PIR; B4776; B44776.
DR PIR; S00727; S00727.
DR PIR; S35745; S35745.
DR HSSP; Q9H2C9; IM17.
DR SMR; Q85468; 121-444.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008266; Tyr_pkinase.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Transferase;
KW Tyrosine-protein kinase.

FT NON_TER 1
SQ SEQUENCE 545 AA; 60899 MW; 140DCB8CCA0F8AF4 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 545;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLQETELV 9
DB 106 RLQERELV 114
|||||

RESULT 15
Q85714_AVEVR PRELIMINARY; PRT; 567 AA.
AC Q85714;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE V-erbB protein (Fragment).
DE Namesv-erbB;
OS Avian rous-associated virus type 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Alpharetrovirus.
OX NCBI_TaxID=11950;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94203659; PubMed=8152791;
RA Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
RA Johnsson A., Beug H.;
RT "Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT evolution of distinct viral genomes carrying mutant v-erbB genes with
RT different transforming capacities.";
RL Oncogene 9:1307-1320(1994).
DR EMBL; S69372; AAC60727.1; -; Genomic_RNA.
DR HSSP; Q9H2C9; IM17.
DR SMR; Q85714; 121-444.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Transferase;
KW Tyrosine-protein kinase.
FT NON_TER 567
SQ SEQUENCE 567 AA; 63391 MW; C6D9CBA7ADF725E1 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 567;
Best Local Similarity 88.9%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLQETELV 9
DB 106 RLQERELV 114
|||||

Search completed: March 1, 2006, 02:50:48
Job time : 229 secs

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OM protein - protein search, using sw model

Run on: March 1, 2006, 03:02:52 ; Search time 19 Seconds
(without alignments)
7.052 Million cell updates/sec

Title: US-09-583-200f-22
Perfect score: 41
Sequence: 1 RLLQETELV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pap.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW PUB.pap.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW PUB.pap.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW PUB.pap.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW PUB.pap.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW PUB.pap.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW PUB.pap.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	7	US-11-033-039-608
2	41	100.0	9	7	US-11-033-039-614
3	41	100.0	1255	6	US-10-770-726-62
4	41	100.0	1255	7	US-11-022-562-213
5	41	100.0	1255	7	US-11-113-202-10
6	41	100.0	1255	7	US-11-033-039-553
7	41	100.0	1255	7	US-11-155-288-9
8	41	100.0	1255	7	US-11-202-516-4
9	41	100.0	1255	7	US-11-175-405-2
10	41	100.0	1258	7	US-11-033-039-930
11	35	85.4	943	7	US-11-113-202-8
12	35	85.4	1210	7	US-11-113-202-6
13	35	85.4	1210	7	US-11-145-566-1
14	32	78.0	738	7	US-11-140-625-11
15	32	78.0	738	7	US-11-140-625-13
16	32	78.0	740	7	US-11-140-625-12
17	31	75.6	1308	6	US-10-912-971-12
18	31	75.6	1308	7	US-11-113-202-16
19	29	70.7	549	6	US-10-467-657-4612
20	29	70.7	549	6	US-10-467-657-7190
21	29	70.7	754	7	US-11-140-625-10
22	29	70.7	3674	7	US-11-000-463-454
23	28	68.3	209	6	US-10-519-390-3
24	28	68.3	209	7	US-11-176-830-203
25	28	68.3	209	7	US-11-176-830-401

26	28	68.3	209	7	US-11-176-830-402	Sequence 402, App
27	28	68.3	209	7	US-11-176-830-403	Sequence 403, App
28	28	68.3	209	7	US-11-176-830-404	Sequence 404, App
29	28	68.3	209	7	US-11-176-830-405	Sequence 405, App
30	28	68.3	209	7	US-11-176-830-406	Sequence 406, App
31	28	68.3	209	7	US-11-176-830-407	Sequence 407, App
32	28	68.3	209	7	US-11-176-830-408	Sequence 408, App
33	28	68.3	209	7	US-11-176-830-409	Sequence 409, App
34	28	68.3	209	7	US-11-176-830-410	Sequence 410, App
35	28	68.3	209	7	US-11-176-830-411	Sequence 411, App
36	28	68.3	209	7	US-11-176-830-412	Sequence 412, App
37	28	68.3	209	7	US-11-176-830-413	Sequence 413, App
38	28	68.3	209	7	US-11-176-830-414	Sequence 414, App
39	28	68.3	209	7	US-11-176-830-415	Sequence 415, App
40	28	68.3	209	7	US-11-176-830-416	Sequence 416, App
41	28	68.3	209	7	US-11-176-830-417	Sequence 417, App
42	28	68.3	209	7	US-11-176-830-418	Sequence 418, App
43	28	68.3	209	7	US-11-176-830-419	Sequence 419, App
44	28	68.3	209	7	US-11-176-830-420	Sequence 420, App
45	28	68.3	209	7	US-11-176-830-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-11-033-039-608
; Sequence 608, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 608
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-608

Query Match 100.0%; Score 41; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
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Db 1 RLLQETELV 9

RESULT 2
US-11-033-039-614
; Sequence 614, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-614

Query Match 100.0%; Score 41; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
DB 1 RLLQETELV 9

RESULT 3

US-10-770-726-62
; Sequence 62, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-62

Query Match 100.0%; Score 41; DB 6; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
DB 689 RLLQETELV 697

RESULT 4

US-11-022-562-213
; Sequence 213, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-562-213

Query Match 100.0%; Score 41; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
DB 689 RLLQETELV 697

RESULT 5

US-11-113-202-10
; Sequence 10, Application US/11113202
; Publication No. US20050272637A1
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail M.
; APPLICANT: Shamieh, Lara
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING SIGNALING BY IGF-1
; FILE REFERENCE: 49321-136
; CURRENT APPLICATION NUMBER: US/11/113,202
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/590,473
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 60/564,893
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-202-10

Query Match 100.0%; Score 41; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9
DB 689 RLLQETELV 697

RESULT 6

US-11-033-039-553
; Sequence 553, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 553
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-553

Query Match 100.0%; Score 41; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLQETELV 9

Db 689 RLLOETELV 697
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RESULT 7
US-11-155-288-9
; Sequence 9, Application US/111155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-9

Query Match 100.0%; Score 41; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
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Db 689 RLLOETELV 697

RESULT 8
US-11-202-516-4
; Sequence 4, Application US/11202516
; Publication No. US20060008465A1
; GENERAL INFORMATION:
; APPLICANT: Steinna, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Dalum, Iben
; APPLICANT: Haaning, Jesper
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; APPLICANT: Rasmussen, Peter
; TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
; FILE REFERENCE: 4614-0107PUS2
; CURRENT APPLICATION NUMBER: US/11/202,516
; PRIOR FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US 09/806,703
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/DK99/00525
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: DK 1998 01261
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: US 60/105,011
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-202-516-4

Query Match 100.0%; Score 41; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
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Db 689 RLLOETELV 697

RESULT 9
US-11-175-405-2
; Sequence 2, Application US/11175405
; Publication No. US20060019344A1
; GENERAL INFORMATION:
; APPLICANT: STUART, SUSAN G.
; APPLICANT: MONAHAN, JOHN J.
; APPLICANT: LANGTON, BEATRICE CLAUDIA
; APPLICANT: HANCOCK, MIRIAM E.C.
; APPLICANT: CHAO, LORRINE A.
; APPLICANT: BLUFORD, PETER
; TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
; FILE REFERENCE: BEBIO-111-C1
; CURRENT APPLICATION NUMBER: US/11/175,405
; PRIOR FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-405-2

Query Match 100.0%; Score 41; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
|||||

Db 689 RLLOETELV 697

RESULT 10
US-11-033-039-930
; Sequence 930, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 930
; LENGTH: 1258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-930

Query Match 100.0%; Score 41; DB 7; Length 1258;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
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Db 689 RLLOETELV 697

RESULT 11
US-11-113-202-8

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; Sequence 8, Application US/11113202
; Publication No. US20050272637A1
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail M.
; APPLICANT: Shamieh, Lara
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING SIGNALING BY IGF-1
; TITLE OF INVENTION: RECEPTOR AND ERBB RECEPTORS
; FILE REFERENCE: 49321-136
; CURRENT APPLICATION NUMBER: US/11/113,202
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/590,473
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 60/564,893
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-202-8

Query Match      85.4%; Score 35; DB 7; Length 943;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RLLQETELV 9
Db      414 RLLQERELV 422

RESULT 12
US-11-113-202-6
; Sequence 6, Application US/11113202
; Publication No. US20050272637A1
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail M.
; APPLICANT: Shamieh, Lara
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING SIGNALING BY IGF-1
; TITLE OF INVENTION: RECEPTOR AND ERBB RECEPTORS
; FILE REFERENCE: 49321-136
; CURRENT APPLICATION NUMBER: US/11/113,202
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/590,473
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 60/564,893
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-202-6

Query Match      85.4%; Score 35; DB 7; Length 1210;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RLLQETELV 9
Db      681 RLLQERELV 689

RESULT 13
US-11-145-566-1
; Sequence 1, Application US/11145566
; Publication No. US20050272083A1
; GENERAL INFORMATION:
; APPLICANT: SOMASEKAR SESHAGIRI
; TITLE OF INVENTION: EGFR Mutations
; FILE REFERENCE: 39766-0153
; CURRENT APPLICATION NUMBER: US/11/145,566
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; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,425
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/635,344
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US 60/666,068
; PRIOR FILING DATE: 2005-03-28
; NUMBER OF SEQ ID NOS: 60
; SEQ ID NO 1
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-566-1

Query Match      85.4%; Score 35; DB 7; Length 1210;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RLLQETELV 9
Db      681 RLLQERELV 689

RESULT 14
US-11-140-625-11
; Sequence 11, Application US/11140625
; Publication No. US20060026706A1
; GENERAL INFORMATION:
; APPLICANT: Van Wezel, Gilles P.
; APPLICANT: Vijgenboom, Erik
; TITLE OF INVENTION: A method for marker-less integration of a sequence of interest
; TITLE OF INVENTION: into the genome of a cell
; FILE REFERENCE: P62377SUS00
; CURRENT APPLICATION NUMBER: US/11/140,625
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: EP 02080000.9
; PRIOR FILING DATE: 2002-11-28
; PRIOR APPLICATION NUMBER: PCT/NL2003/000835
; PRIOR FILING DATE: 2003-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ETR1 homologue derived from Nicotiana tabacum
US-11-140-625-11

Query Match      78.0%; Score 32; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLQETEL 8
Db      366 LLQETEL 372

RESULT 15
US-11-140-625-13
; Sequence 13, Application US/11140625
; Publication No. US20060026706A1
; GENERAL INFORMATION:
; APPLICANT: Van Wezel, Gilles P.
; APPLICANT: Vijgenboom, Erik
; TITLE OF INVENTION: A method for marker-less integration of a sequence of interest
; TITLE OF INVENTION: into the genome of a cell
; FILE REFERENCE: P62377SUS00
; CURRENT APPLICATION NUMBER: US/11/140,625
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: EP 02080000.9
; PRIOR FILING DATE: 2002-11-28
; PRIOR APPLICATION NUMBER: PCT/NL2003/000835
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; PRIOR FILING DATE: 2003-11-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ETR1 homologue derived from Arabidopsis thaliana
US-11-140-625-13

Query Match 78.0%; Score 32; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LQOETEL 8
| | | | |
Db 368 LQOETEL 374

Search completed: March 1, 2006, 03:05:52
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: March 1, 2006, 03:02:17 ; Search time 164 Seconds
(without alignments)
22.930 Million cell updates/sec

Title: US-09-583-200F-22
Perfect score: 41
Sequence: 1 RLQTELV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	9	2	US-08-812-393A-52
2	41	100.0	9	3	US-09-354-533-6
3	41	100.0	9	3	US-09-894-018-320
4	41	100.0	9	3	US-09-774-681-52
5	41	100.0	9	4	US-10-001-546-26
6	41	100.0	9	4	US-10-080-013-40
7	41	100.0	9	4	US-10-080-013-41
8	41	100.0	9	4	US-10-245-871-608
9	41	100.0	9	4	US-10-245-871-614
10	41	100.0	9	4	US-10-149-138-671
11	41	100.0	9	4	US-10-149-138-2276
12	41	100.0	9	4	US-10-149-138-4420
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15	41	100.0	9	4	US-10-253-286-614
16	41	100.0	9	4	US-10-289-566-41
17	41	100.0	9	4	US-10-333-430-65
18	41	100.0	9	4	US-10-647-005-6
19	41	100.0	9	4	US-10-149-138-671
20	41	100.0	9	4	US-10-149-138-2276
21	41	100.0	9	4	US-10-149-138-4420
22	41	100.0	9	5	US-10-474-960A-320
23	41	100.0	9	5	US-10-862-213A-9
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25	41	100.0	15	3	US-09-354-533-40
26	41	100.0	15	4	US-10-149-138-3869
27	41	100.0	15	4	US-10-149-138-3927

28	41	100.0	15	4	US-10-149-138-4530	Sequence 4530, Ap
29	41	100.0	15	4	US-10-647-005-40	Sequence 40, Appl
30	41	100.0	15	4	US-10-149-138-3869	Sequence 3869, Ap
31	41	100.0	15	4	US-10-149-138-3927	Sequence 3927, Ap
32	41	100.0	15	4	US-10-149-138-4530	Sequence 4530, Ap
33	41	100.0	15	6	US-11-121-347-40	Sequence 40, Appl
34	41	100.0	16	3	US-09-354-533-63	Sequence 63, Appl
35	41	100.0	16	4	US-10-647-005-63	Sequence 63, Appl
36	41	100.0	16	5	US-10-862-213A-6	Sequence 6, Appl
37	41	100.0	16	6	US-11-121-347-63	Sequence 63, Appl
38	41	100.0	36	4	US-10-392-113-44	Sequence 44, Appl
39	41	100.0	126	4	US-10-333-430-70	Sequence 70, Appl
40	41	100.0	144	3	US-09-894-018-129	Sequence 129, App
41	41	100.0	144	5	US-10-474-960A-129	Sequence 129, App
42	41	100.0	147	3	US-09-894-018-131	Sequence 131, App
43	41	100.0	147	5	US-10-474-960A-131	Sequence 131, App
44	41	100.0	148	3	US-09-894-018-127	Sequence 127, App
45	41	100.0	148	5	US-10-474-960A-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-812-393A-52
; Sequence 52, Application US/08812393A
; Publication No. US20010007152A1
; GENERAL INFORMATION:
; APPLICANT: SHERMAN, Linda A.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING
; TITLE OF INVENTION: T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,393A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 31333-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0169
; TELEX:
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-812-393A-52

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

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QY 1 RLLOETELV 9
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Db 1 RLLOETELV 9

RESULT 2
US-09-354-533-6
; Sequence 6, Application US/09354533
; Publication No. US20020055614A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; DISG, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-354-533-6

Query Match 100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
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Db 1 RLLOETELV 9

RESULT 3
US-09-894-018-320
; Sequence 320, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Deniaw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
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; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
; US-09-894-018-320

Query Match 100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
    |||||
Db 1 RLLOETELV 9

RESULT 4
US-09-774-681-52
; Sequence 52, Application US/09774681
; Publication No. US20030208780A1
; GENERAL INFORMATION:
; APPLICANT: Sunol Molecular Corporation
; APPLICANT: Sherman, Linda
; APPLICANT: Lustgarten, Joseph
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL
; TITLE OF INVENTION: RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
; FILE REFERENCE: 31333-20001.01
; CURRENT APPLICATION NUMBER: US/09/774,681
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 08/812,393
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: US 60/012,845
; PRIOR FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide
; US-09-774-681-52

Query Match 100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOETELV 9
    |||||
Db 1 RLLOETELV 9

RESULT 5
US-10-001-546-26
; Sequence 26, Application US/10001546
; Publication No. US20030027766A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: FISK, BRYAN A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; FILE REFERENCE: UTSC:390USC2
; CURRENT APPLICATION NUMBER: US/10/001,546
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 08/403,459
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; PRIOR FILING DATE: 1995-03-14
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-001-546-26

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
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DB 1 RLLOQETELV 9

RESULT 6
US-10-080-013-40
; Sequence 40, Application US/10080013
; Publication No. US2003007248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-40

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
| | | | | | | | |
DB 1 RLLOQETELV 9

RESULT 7
US-10-080-013-41
; Sequence 41, Application US/10080013
; Publication No. US2003007248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-080-013-41

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
| | | | | | | | |
DB 1 RLLOQETELV 9

RESULT 8
US-10-245-871-608
; Sequence 608, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 608
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-608

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
| | | | | | | | |
DB 1 RLLOQETELV 9

RESULT 9
US-10-245-871-614
; Sequence 614, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-614

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
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Db 1 RLLQETELV 9

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-10-149-138-671
; Sequence 671, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 671
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-671

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9
| | | | | | | | |
Db 1 RLLQETELV 9

RESULT 11
US-10-149-138-2276
; Sequence 2276, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2276
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2276

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9
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Db 1 RLLQETELV 9

RESULT 12
US-10-149-138-4420
; Sequence 4420, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4420
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4420

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLQETELV 9
| | | | | | | | |
Db 1 RLLQETELV 9

RESULT 13
US-10-447-161-88
; Sequence 88, Application US/10447161
; Publication No. US2004002314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: WO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-88

Query Match 100.0%; Score 41; DB 4; Length 9;

Job time : 165 secs

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQETELV 9
| | | | |
Db 1 RLQETELV 9

RESULT 14

US-10-253-286-608
; Sequence 608, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; FILE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 608
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-608

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQETELV 9
| | | | |
Db 1 RLQETELV 9

RESULT 15

US-10-253-286-614
; Sequence 614, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; FILE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 614
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-614

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLQETELV 9
| | | | |
Db 1 RLQETELV 9

Search completed: March 1, 2006, 03:05:29

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OM protein - protein search, using sw model

Run on: March 1, 2006, 02:51:02 ; Search time 47 Seconds
(without alignments)
15.832 Million cell updates/sec

Title: US-09-583-200F-22
Perfect score: 41
Sequence: 1 RLLOETELV 9

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/pCTUS COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	41	100.0	9	1 US-08-467-083-6	Sequence 6, Appli
2	41	100.0	9	1 US-08-414-417B-6	Sequence 6, Appli
3	41	100.0	9	1 US-08-486-348A-6	Sequence 6, Appli
4	41	100.0	9	1 US-08-468-545B-6	Sequence 6, Appli
5	41	100.0	9	2 US-08-466-680B-6	Sequence 6, Appli
6	41	100.0	9	2 US-08-403-459-26	Sequence 26, Appli
7	41	100.0	9	2 US-09-543-608A-7	Sequence 7, Appli
8	41	100.0	9	2 US-09-354-533-6	Sequence 6, Appli
9	41	100.0	15	1 US-08-467-083-40	Sequence 40, Appli
10	41	100.0	15	1 US-08-414-417B-40	Sequence 40, Appli
11	41	100.0	15	1 US-08-486-348A-40	Sequence 40, Appli
12	41	100.0	15	1 US-08-468-545B-40	Sequence 40, Appli
13	41	100.0	15	2 US-08-466-680B-40	Sequence 40, Appli
14	41	100.0	15	2 US-09-354-533-40	Sequence 40, Appli
15	41	100.0	16	1 US-08-467-083-63	Sequence 63, Appli
16	41	100.0	16	1 US-08-414-417B-63	Sequence 63, Appli
17	41	100.0	16	1 US-08-486-348A-63	Sequence 63, Appli
18	41	100.0	16	1 US-08-468-545B-63	Sequence 63, Appli
19	41	100.0	16	2 US-08-466-680B-63	Sequence 63, Appli
20	41	100.0	16	2 US-09-354-533-63	Sequence 63, Appli
21	41	100.0	580	1 US-08-414-417B-69	Sequence 69, Appli
22	41	100.0	580	1 US-08-486-348A-69	Sequence 69, Appli
23	41	100.0	580	1 US-08-468-545B-69	Sequence 69, Appli
24	41	100.0	580	2 US-08-466-680B-69	Sequence 69, Appli
25	41	100.0	580	2 US-09-354-533-69	Sequence 69, Appli
26	41	100.0	1255	1 US-08-467-083-68	Sequence 68, Appli
27	41	100.0	1255	1 US-08-414-417B-68	Sequence 68, Appli

28	41	100.0	1255	1 US-08-484-438-8	Sequence 8, Appli
29	41	100.0	1255	1 US-08-486-348A-68	Sequence 68, Appli
30	41	100.0	1255	1 US-08-625-101-2	Sequence 2, Appli
31	41	100.0	1255	1 US-08-468-545B-68	Sequence 68, Appli
32	41	100.0	1255	1 US-08-356-786-2	Sequence 2, Appli
33	41	100.0	1255	2 US-08-466-680B-68	Sequence 68, Appli
34	41	100.0	1255	2 US-09-527-487-2	Sequence 2, Appli
35	41	100.0	1255	2 US-09-811-115-3	Sequence 3, Appli
36	41	100.0	1255	2 US-09-354-533-68	Sequence 68, Appli
37	41	100.0	1255	2 US-09-441-411-6	Sequence 6, Appli
38	41	100.0	1255	2 US-09-167-516-2	Sequence 2, Appli
39	35	85.4	391	2 US-09-482-273-151	Sequence 151, App
40	35	85.4	414	2 US-09-482-273-239	Sequence 239, App
41	35	85.4	1210	1 US-08-484-438-7	Sequence 7, Appli
42	35	85.4	1210	1 US-08-475-035-4	Sequence 4, Appli
43	35	85.4	1210	2 US-09-715-249-2	Sequence 2, Appli
44	35	85.4	1210	2 US-09-723-307-67	Sequence 67, Appli
45	32	78.0	97	2 US-09-489-039A-13027	Sequence 13027, A

ALIGNMENTS

RESULT 1
US-08-467-083-6
; Sequence 6, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-467-083-6

Query Match 100.0%; Score 41; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLOETELV 9

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Db      1 RLLQETELV 9
|||||
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-486-348A-6

Query Match      100.0%; Score 41; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLLQETELV 9
|||||
Db      1 RLLQETELV 9
|||||

RESULT 4
US-08-468-545B-6
; Sequence 6, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-6

Query Match      100.0%; Score 41; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLLQETELV 9
|||||
Db      1 RLLQETELV 9
|||||

RESULT 3
US-08-486-348A-6
; Sequence 6, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
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Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 RLQETELV 9
|||||
Db 1 RLQETELV 9

RESULT 5
US-08-466-680B-6
; Sequence 6, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-466-680B-6

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
|||||
Db 1 RLQETELV 9

RESULT 6
US-08-459-26
; Sequence 26, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantin G.
; APPLICANT: Fisk, Bryan A.
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,459
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSC:390/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-459-26

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
|||||
Db 1 RLQETELV 9

RESULT 7
US-09-543-608A-7
; Sequence 7, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HER2/neu.689
US-09-543-608A-7

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLQETELV 9
|||||
Db 1 RLQETELV 9

RESULT 8
US-09-354-533-6
; Sequence 6, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 622-4901
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-354-533-6
Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLQETELV 9
Db 1 RLQETELV 9
RESULT 9
US-08-467-083-40
; Sequence 40, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-467-083-40
Query Match 100.0%; Score 41; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RLQETELV 9
Db 6 RLQETELV 14
RESULT 10
US-08-414-417B-40
; Sequence 40, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-414-417B-40

Query Match 100.0%; Score 41; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
DB 6 RLLOQETELV 14

RESULT 11

US-08-486-348A-40
; Sequence 40, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disig, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-486-348A-40

Query Match 100.0%; Score 41; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
DB 6 RLLOQETELV 14

RESULT 12

US-08-468-545B-40
; Sequence 40, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disig, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-545B-40

Query Match 100.0%; Score 41; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLLOQETELV 9
DB 6 RLLOQETELV 14

RESULT 13

US-08-466-680B-40
; Sequence 40, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disig, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-40

INFORMATION FOR SEQ ID NO: 40:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-466-680B-40

Query Match      100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLLQETELV 9
Db      6 RLLQETELV 14

RESULT 14
US-09-354-533-40
; Sequence 40, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; DISIS, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-354-533-40

Query Match      100.0%; Score 41; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLLQETELV 9
Db      6 RLLQETELV 14

RESULT 15
US-08-467-083-63
; Sequence 63, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; DISIS, Mary L.
```

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; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-467-083-63

Query Match      100.0%; Score 41; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLLQETELV 9
Db      2 RLLQETELV 10

Search completed: March 1, 2006, 02:52:24
Job time : 48 secs
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